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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 12:54:35 ; Search time 19513.3 Seconds
(without alignments)
17420.151 Million cell updates/sec

Title: US-10-781-979-1

Perfect score: 5980

Sequence: 1 tacatgcaatacataaagag.....ttctaaagaagcctctgtat 5980

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5980	100.0	5980	6	CQ868311 Sequence
2	2705	45.2	3746	1	AB074414 Bacillus
3	2223.4	37.2	4100	1	AB112346 Bacillus
4	2082	34.8	2082	6	CQ868312 Sequence
5	2073	34.7	2073	6	CQ868314 Sequence
6	1686	28.2	1686	6	CQ868316 Sequence
7	1526.4	25.5	3727	1	AB074413 Bacillus
8	1038.8	17.4	3752	1	AB125059 Bacillus
9	967	16.2	4391	1	BTJEG65
10	966.2	16.2	3931	1	AB161456
11	935.4	15.6	3668	1	AB185105 Bacillus
12	891.6	14.9	3642	1	AB193814 Bacillus
13	860.8	14.4	127923	1	BTPTOXIS
14	855	14.3	2145	6	CQ868324 Sequence
15	790.6	13.2	4186	1	BACISRH3
16	790.6	13.2	4186	6	E01905
17	789	13.2	3684	1	BTITOX
18	789	13.2	3684	1	BTTOXD2

19	789	13.2	3684	6	I08884	108884 Sequence 2
20	787.4	13.2	3535	6	I06096	106096 Sequence 2
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22	776.2	13.0	127923	1	BTPTOXIS	AL731825 Bacillus
23	774.6	13.0	4934	6	E01676	E01676 DNA sequenc
24	769.8	12.9	4451	6	I08083	I08083 Sequence 1
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26	768.6	12.9	4056	1	BACCRD2	M20242 B.thuringie
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33	400.4	6.7	3756	6	E00614	E00614 DNA encodin
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36	390	6.5	4359	6	AX670917	AX670917 Sequence
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ALIGNMENTS

RESULT 1
LOCUS CQ868311
DEFINITION Sequence 12 from Patent WO2004074462.
ACCESSION CQ868311
VERSION CQ868311.1 GI:51998357
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITILE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 12 02-SEP-2004;
Athenix Corporation (US)
FEATURES
Location/Qualifiers
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Db	61	TATTTGTAGAAACATTTGTACAGGAATAC	100.0%	5980	5980	0	0	0	0	0
QY	121	CTAACATATATTTATTAGTGCTTAA	100.0%	5980	5980	0	0	0	0	0
Db	121	CTAACATATATTTATTAGTGCTTAA	100.0%	5980	5980	0	0	0	0	0
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241	Db	CGCCAAAACAGATATCCTTTTGCAAAATAATCGGGATATGTCTACTATGTCTTGGAAATGATT	300
301	Qy	GTCCAGGAAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAAACAAGTATTGGGA	360
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361	Qy	TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATATACACTATTATCAA	420
361	Db	TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATATACACTATTATCAA	420
421	Qy	TAAATAGGAAACTAAATTTCCGACTAAATCGTCAAACTGTGCAGCACTTTCTATATGTGATT	480
421	Db	TAAATAGGAAACTAAATTTCCGACTAAATCGTCAAACTGTGCAGCACTTTCTATATGTGATT	480
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481	Db	TATTATCTATAATTCGTAAGAGAGTAGCCGATAGTGTTTTAAAGTGATGCGATTGCAGATT	540
541	Qy	TTGACGGTAAATTCGAAAAATATATAGAGAGTATTAATCTTCTATCTTTGGGGCTTGGCTTA	600
541	Db	TTGACGGTAAATTCGAAAAATATATAGAGAGTATTAATCTTCTATCTTTGGGGCTTGGCTTA	600
601	Qy	AAGACGGTAAACCACTTTCAAAAGACAATAATCTCGATATCGGACAATTAAGTTTATTATT	660
601	Db	AAGACGGTAAACCACTTTCAAAAGACAATAATCTCGATATCGGACAATTAAGTTTATTATT	660
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661	Db	TTAACTTTTCCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCAATTTGTCAAGAAACAATG	720
721	Qy	CTCAAGTATTGTTATTACTTCTTTTGGCAAGCTGCAAAATGTGCACTTATTAATATAA	780
721	Db	CTCAAGTATTGTTATTACTTCTTTTGGCAAGCTGCAAAATGTGCACTTATTAATATAA	780
781	Qy	GGGATGCAGTTCAATATAAGACAAGTGGTCCCATTTTTCAGTGCAGAGAACTGAAGAT	840
781	Db	GGGATGCAGTTCAATATAAGACAAGTGGTCCCATTTTTCAGTGCAGAGAACTGAAGAT	840
841	Qy	CGGAAATTAATATCACCTTAACAGTGGTTGTGATTTTACCGGTGATTAATATGACGCGATTAA	900
841	Db	CGGAAATTAATATCACCTTAACAGTGGTTGTGATTTTACCGGTGATTAATATGACGCGATTAA	900
901	Qy	AATGCCAAAACGGCAGAGTATACCAATTAATTTGTTTATATTCGGTATCAGGTAGGTTAAATC	960
901	Db	AATGCCAAAACGGCAGAGTATACCAATTAATTTGTTTATATTCGGTATCAGGTAGGTTAAATC	960
961	Qy	AGATAAAACAGGGGGGACAGGTCTGCACACTTGGTCGAAATTTTAAATAATTCGTTAGAG	1020
961	Db	AGATAAAACAGGGGGGACAGGTCTGCACACTTGGTCGAAATTTTAAATAATTCGTTAGAG	1020
1021	Qy	AAATGACGTTTGGCGGTATTCGATTAATTCGCTATATTTCCAACTTATGATTTTTCAGAAAT	1080
1021	Db	AAATGACGTTTGGCGGTATTCGATTAATTCGCTATATTTCCAACTTATGATTTTTCAGAAAT	1080
1081	Qy	ATCCATTTGCCAACACACATGTAGAGTTGACTAGGGAAAAATTTATACAGATGCAGTGGGATATT	1140
1081	Db	ATCCATTTGCCAACACACATGTAGAGTTGACTAGGGAAAAATTTATACAGATGCAGTGGGATATT	1140
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1141	Db	CATCGGAACTTATAGTTGGTTACGGAAATTCGGCTTAATCTTTTAAATGGGTTAGAGCTTA	1200
1201	Qy	ATGGAAACACGGGGACCTGGTTTACTTGGCTTTAGCAAAATTAAGGTATATATAATGAGT	1260
1201	Db	ATGGAAACACGGGGACCTGGTTTACTTGGCTTTAGCAAAATTAAGGTATATATAATGAGT	1260
1261	Qy	ATGTTTTCAGAGATATTTTCCCGCTGGGTAGGAACTCGTCAATTAATGAAGACTACACAAAGG	1320
1261	Db	ATGTTTTCAGAGATATTTTCCCGCTGGGTAGGAACTCGTCAATTAATGAAGACTACACAAAGG	1320

QY	1321	GTAA	CGGTATTTTT	CAAC	GTATGTCT	TGGA	AAC	CTAC	GAGTAA	TGATCTAC	GTAATATT	TGATTT	1381
DB	1321	GTAA	CGGTATTTTT	CAAC	GTATGTCT	TGGA	AAC	CTAC	GAGTAA	TGATCTAC	GTAATATT	TGATTT	1380
QY	1381	TTCA	GAATGCCG	ATGTATATA	AAAA	TACTTT	CATT	AGCTAT	CATGA	CACTAG	TAGTAGG	AGAGA	1440
DB	1381	TTCA	GAATGCCG	ATGTATATA	AAAA	TACTTT	CATT	AGCTAT	CATGA	CACTAG	TAGTAGG	AGAGA	1440
QY	1441	CTAC	CGCTAG	ACAGAG	TATCGT	GT	TTTCAA	AGGCAG	ATTTTCG	TAGGTA	AGGGGAC	CTCG	1500
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DB	1501	ATTT	AAAAATTAT	GATG	CAGG	TAAATA	TG	GGCTA	GAGGAT	GCAAT	TGAATCT	ACGTTC	1560
QY	1561	CAC	TGTATTG	CACTCTAA	TGTG	TTAG	AGGAC	CCCTCT	CATAG	ATTAT	CAAA	TGCGGCAT	1620
DB	1561	CAC	TGTATTG	CACTCTAA	TGTG	TTAG	AGGAC	CCCTCT	CATAG	ATTAT	CAAA	TGCGGCAT	1620
QY	1621	GTG	TTGTATAT	TGAA	ACTCC	AGAG	TTAA	CGTATAT	TG	GTGGA	CACATAC	AAAGTTTAA	1680
DB	1621	GTG	TTGTATAT	TGAA	ACTCC	AGAG	TTAA	CGTATAT	TG	GTGGA	CACATAC	AAAGTTTAA	1680
QY	1681	GTG	AAAAATA	TAA	TTTGA	AGC	CAATCA	AAAT	TAC	CAAA	TACCG	CGGTGA	1740
DB	1681	GTG	AAAAATA	TAA	TTTGA	AGC	CAATCA	AAAT	TAC	CAAA	TACCG	CGGTGA	1740
QY	1741	TTCA	AAATTTAT	CTTG	CTAA	TG	CCCTATAC	CTAT	GTAT	TAATA	AAAG	CACTCATAC	1800
DB	1741	TTCA	AAATTTAT	CTTG	CTAA	TG	CCCTATAC	CTAT	GTAT	TAATA	AAAG	CACTCATAC	1800
QY	1801	ATTT	TAATCCG	TTTTTAA	GA	ACAA	ATTC	AGAG	TATA	ACG	CAGTTAT	G	1860
DB	1801	ATTT	TAATCCG	TTTTTAA	GA	ACAA	ATTC	AGAG	TATA	ACG	CAGTTAT	G	1860
QY	1861	TTAG	ATTGATTATTA	TATA	CA	AAAA	CTTG	CA	GGA	CAAA	AGTTAC	CCGTATTT	1920
DB	1861	TTAG	ATTGATTATTA	TATA	CA	AAAA	CTTG	CA	GGA	CAAA	AGTTAC	CCGTATTT	1920
QY	1921	CTG	CAGATAA	AGCTGCTTTCT	T	TAG	TGTATATCTTT	TAT	CCAG	AGGTTGG	GGTTCA	AATC	1980
DB	1921	CTG	CAGATAA	AGCTGCTTTCT	T	TAG	TGTATATCTTT	TAT	CCAG	AGGTTGG	GGTTCA	AATC	1980
QY	1981	GT	TTGTATCG	CTTG	AAAA	CTTTACT	CTG	CAAT	TATG	ACG	ATTTAA	ATA	2040
DB	1981	GT	TTGTATCG	CTTG	AAAA	CTTTACT	CTG	CAAT	TATG	ACG	ATTTAA	ATA	2040
QY	2041	TTAA	TTCCGTG	AAATPAT	CAC	AC	CTTCA	ATTAC	TAG	TTCA	AA	CAATTC	2100
DB	2041	TTAA	TTCCGTG	AAATPAT	CAC	AC	CTTCA	ATTAC	TAG	TTCA	AA	CAATTC	2100
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Qy	5941	TCAAAATATCGTTTAAAGCCTCTTAAAGCCCTCTCTGAT	5980
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LOCUS	AB074414	3746 bp	DNA linear BCT 14-JUN-2003
DEFINITION	AB074414	Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.	
ACCESSION	AB074414	GI:16945771	
VERSION	AB074414.1		
KEYWORDS		Bacillus thuringiensis serovar aizawai	
SOURCE		Bacillus thuringiensis serovar aizawai	
ORGANISM		Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.	
REFERENCE		1	
AUTHORS		Ito, T., Sahara, K., Asano, S. and Bando, H.	
TITLE		Cloning and Expression of Novel Crystall Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 3746)	
AUTHORS		Ito, T., Sahara, K., Asano, S. and Bando, H.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Kita-9Jyou Nishi-9chome, Kita-ku, Sapporo-shi, Hokkaido 060-8589, Japan	
FEATURES		(E-mail: ito-teabs.agr.hokudai.ac.jp, Tel:81-011-716-2487)	
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ORIGIN

Query Match 45.2%; Score 2705; DB 1; Length 3746;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 3223; Conservative 0; Mismatches 505; Indels 95; Gaps 12;
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QY 239 TAGCCAAAACAGATATCTTTTTCGAAATAATCGGATATGCTACTATGTCCTTGGAAATGA 298
DB 61 TATGCCAAACAGATATCTTTTTCGAAATAATCGGATATGCTACTATGTCCTTCAATGA 120
QY 299 TTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCCGAAACGATAACAAAGTATGG 358
DB 121 TTGTCAAGGAATCTCATGGGATGAAATTTGGGAATCAGCCGAAACGATAACAAAGTATGG 180
QY 359 GATAAATCTTATAGATTTGTGTAGAACCTAGTTTGGGTAATTAATACACTATATAC 418
DB 181 GATAGATCTTATAGAGTTTGTGTAGAACCTAGTTTGGGTAATTAATACACTATATTTTC 240
QY 419 AATAATAGGAAACTAATTCGGAATCTGCTCAAACTGCTCAGCACTTTCTATATGTGA 478
DB 241 AATAATAGGAAACTAATTCGGAATCTGCTCAAACTGCTCAGCACTTTCTATATGTGA 300
QY 479 TTTATATCTATATTCGTAAGAGGTPAGCCGATAGTGTGTTTAAAGTGATGCGATT ---GC 535
DB 301 TTTATATCTATATTCGTAAGAGGTPAGCCGATAGTGTGTTTAAAGTGATGCGATTTCGCGAG 360
QY 536 AGATTTTGAGGTAAATTTGAAATTTATAGAGATATATCTTTCTATCTTGGGCTTG 595
DB 361 ATTTTGGGCGGTAAATTTGAAATTTATAGAGATATATCTTTCTATCTTGGGCTTG 420
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DB QY 660 TAAGATCGGAATTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTACTATGAGC 719
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DB 720 GATTAAATGTAATAATAGCAGAGTATACCGGATTTATTTGTAATATTTGGTATCAGCGGTT 779
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DB 780 TAAATCAATATAAAGAGGGGGGACAGGTCTGACACTTGGGGGAAATTTAAATAAATTTTC 839
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DB 960 GATATTCATCAGGAATCTTATAGCTGGTTAAAGTATTTGGACCGGTGCTTTTAAATCGTTAG 1019
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QY 1435 GAGAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGGCAAGTATTTTCGTAGGCTAGGGG 1494
DB 1260 GAGAGATTAACGCTAGACCGGATGCTGTGTTTCACGCTGAGAAATTTTAGTGAGTCAACAG 1319
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DB 1560 CTTTGTATATACGGAT -----ACAGGCCAGGTC 1589
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DB 1590 AAGTCATAGCTGGACCTGCTCATACAGGAGGAAATGTAGTAAGCTTTACCATATTTATTCAC 1649
QY 1852 GTGGCGGAATAGATTGATTATTAATAACAAACTGCAGGACAAAGCTTACCGTATTTTCGTT 1911
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DB 1704 TTCGCTATACAAGTACGAGCAATGGTAGGTACTAGTAGAAAGATGGTCCGCCGAGTTCTA 1763

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3714	AAGGTACATTTTATATAGATAGCATCGAGTTGCTTTGTTATGCAAGGATATGATAACAATA	3773
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RESULT 4					
CQ868312					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
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SOURCE					
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AUTHORS					
TITLE					
JOURNAL					

ORIGIN	FKPEIITPPLPSSNIQMDVEMOANSFQSDVNVVLDKIBFLPSPNTTTTLEYEGERDLEL TKNAVNDLFTN"									
Query Match	34.8%	Score 2082;	DB 6;	Length 2082;						
Best Local Similarity	100.0%;	Pred. No. 0;								
Matches 2082;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;						
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Db	61	AATAACACAATACGCCAAACAGATATCTTTTGCAAATAATACGGGATATGTCTACTATG	120							
Qy	288	TCYTGGNAATGTTTCAGGGNATCTCATGGGATGAATTTGGGAATCAGTCGNAACGATA	347							
Db	121	TCYTGGNAATGTTTCAGGGNATCTCATGGGATGAATTTGGGAATCAGTCGNAACGATA	180							
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Db	181	ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGTGGAATTAAT	240							
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Qy	468	TCTATATGTGATTTATATCTATATAATTCGTAAGAGGATAGCCGATAGTGTTTTAAGTGAT	527							
Db	301	TCTATATGTGATTTATATCTATATAATTCGTAAGAGGATAGCCGATAGTGTTTTAAGTGAT	360							
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Qy	768	TTATTACTATTAGGGATGCAGTTTCAATATAAAGACAAATGGTTCCTATTTTGGAGTGCA	827							
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Qy	828	GAGAAATGAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTTACCGGTGATTAC	887							
Db	661	GAGAAATGAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTTACCGGTGATTAC	720							
Qy	888	TATGACGGATTAATAATGCAAAACGGCAGAGTATACCAATTTATGTTTATATTGGTATCAG	947							
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QY 1548 GAATCTACGTTCCCACTTGTATTGCATCTTAATGGTGTAGAGGACCTCTCATAGATTA 1607
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QY 1728 AAGAGTTATTACCTTCAAAATTTATCTTGCTAATGCTTACCTATGATTAATAAAGCACT 1787
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QY 1788 CATACAGTGGGATTTAATCCGTTTTTTAAGAACAAAATCAGAGTATAACGAGTTTAT 1847
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QY 1848 GCAGTGGCGGAATTAGATTGATTATTAATAACAAACTGCAGGACAAAGTTACCGTATT 1907
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QY 2208 GAAAAACAAAGAACCGGGTGAACGATCTGTGTTTACCAATTA 2249

Db 2041 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTA 2082

RESULT 5
CQ868314
LOCUS CQ868314 2073 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 15 from Patent WO2004074462.
ACCESSION CQ868314
VERSION CQ868314.1 GI:51998360
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

1
Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
Delta-endotoxin genes and methods for their use
Patent: WO 2004074462-A 15 02-SEP-2004;
Athenix Corporation (US)
Location/Qualifiers
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ORIGIN

Query Match 34.7%; Score 2073; DB 6; Length 2073;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 357 GGGATAAATCTTATAGAGTTTGTGTAGAACCTAGTTGGGTGGGAATTAATACACTATTA 416
Db 181 GGGATAAATCTTATAGAGTTTGTGTAGAACCTAGTTGGGTGGGAATTAATACACTATTA 240
QY 417 TCAATAATAGGAAAACCTAATTCGCGACTAATCGTCAAACTGTGTAGCTCAGCACTTTCTATGCT 476
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DEFINITION Sequence 17 from Patent WO2004074462.
ACCESSION CQ868316
VERSION CQ868316.1 GI:51998362
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE

1. Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.
Delta-endotoxin genes and methods for their use
Patent: WO 2004074462-A 17 02-SEP-2004;
Athenix Corporation (US)

FEATURES

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TITLE Cloning and Expression of Novel Crystal Protein Genes cry39A and 39orf2 from *Bacillus thuringiensis* subsp. *aizawai* Bunl-14 Encoding Mosquitocidal Proteins

JOURNAL Insect Biotechnol. Sericulture 71, 123-128 (2002)

REFERENCE 2 (bases 1 to 3727)

AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Applied Bioscience, Kita 9-jyo, Nishi 9-chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail: ito-t@ab.sagr.hokudai.ac.jp, Tel: 81-011-706-2487, Fax: 81-011-706-2487)

COMMENT On Mar 12, 2002 this sequence version replaced gi:16945768.

FEATURES

source

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ORIGIN

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VERSION     Y07603.1  GI:2624004
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SOURCE      Bacillus thuringiensis
ORGANISM    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE   1
AUTHORS     Rosso, M. L. and Delecluse, A.
TITLE       Contribution of the 65-kilodalton protein encoded by the cloned gene cry19A to the mosquitocidal activity of Bacillus thuringiensis subsp. jegathesan
JOURNAL     Appl. Environ. Microbiol. 63 (11), 4449-4455 (1997)
PUBMED      9361431
REFERENCE   2  (bases 1 to 4391)
AUTHORS     Delecluse, A.
TITLE       Direct Submission
JOURNAL     Submitted (20-AUG-1996) A. Delecluse, Institut Pasteur, Unite des Bacteries Entomopathogenes, 25 rue du Dr. Roux, 75724 Paris Cedex 15, FRANCE
REMARK      revised by submitter 16-SEP-1997
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 AB161456
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 ORGANISM Bacillus thuringiensis serovar entomocidus
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
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REFERENCE 1

Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.
 Cloning and Expression of Novel Crystal Protein Genes from *Bacillus*
thuringiensis subsp. *entomocidus* INA288
 Unpublished

REFERENCE 2

(bases 1 to 3931)
 Tomonori, I., Kumiko, Y., Takeishi, I., Ken, S., Shin-ichiro, A. and
 Hisanori, B.
 Direct Submission
 Submitted (30-JAN-2004) Ikeya Tomonori, Graduate School of
 Agriculture, Hokkaido University, Department of Applied Bioscience,
 Kita-9-jo, Nishi-9-chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan
 (E-mail: ikeya@nab.agr.hokudai.ac.jp, Tel. 81-011-706-2487 (ex. 2487),
 Fax: 81-011-706-2487)

FEATURES

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ORIGIN

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DEFINITION

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Accession

AB185105

Version

AB185105.1

Keywords

Source

Organism

3668 bp

DNA

linear

BCT 23-JUL-2004

Bacillus thuringiensis cry24-like, orf281 genes for

delta-endotoxin, hypothetical protein, complete cds.

GI:50539654

Bacillus thuringiensis

Bacillus thuringiensis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

1

Ohgushi,A., Saitoh,H., Wasano,N. and Ohba,M.

Cloning and characterization of novel cry genes from a

mosquitocidal Bacillus thuringiensis serovar sotto strain

Unpublished

2

(bases 1 to 3668)

Ohgushi,A., Saitoh,H., Wasano,N. and Ohba,M.

Direct Submission

Submitted (16-JUL-2004)

Akira Ohgushi, Kyushu University, Graduate

School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka,

Fukuoka 812-8581, Japan (E-mail:ohgushi@rs.kyushu-u.ac.jp,

Tel:81-92-642-3028, Fax:81-92-642-3028)

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ACCESSION AB193814
VERSION AB193814.1 GI:54695304
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.

1 Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.
Identification and characterization of novel cry genes from an
mosquito-specific Bacillus thuringiensis serovar sotto strain
Unpublished
2 (bases 1 to 3642)
Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.
Direct Submission
Submitted (26-OCT-2004) Akira Ohgushi, Kyushu University, Graduate
School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka,
Fukuoka, 812-8581, Japan (E-mail:ohgushi@brs.kyushu-u.ac.jp,
Tel:81-92-642-3028, Fax:81-92-642-3028)

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FEATURES
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ORIGIN

Query Match 14.9%; Score 891.6; DB 1; Length 3642;
Best Local Similarity 66.8%; Pred. No. 2.4e-137;
Matches 1436; Conservative 0; Mismatches 649; Indels 65; Gaps 9;

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KGVHKTRYITLXLSHSDSKAGESEQRDPFPTKATYAKAKFIISAVLQEMNIG
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Best Local Similarity 59.3%; Pred. No. 8.4e-133;
Matches 1757; Conservative 0; Mismatches 1122; Indels 83; Gaps 14;
QY 861 AGTGGTTGTGATTTTACCGGTGATTACTATGACGATTTAAATGCAAAACGGCAGAGTAT 920
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QY 921 ACCAATTTGTTTATTTGTTATCAGTGGTATTAATCAGATAAAACAGGGGGGAC 980
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QY 981 GGTGCTGACACTTGGTCGAAATTTAATAATTTCTGTAGAGAAATGACGTTGGCGGTATTG 1040
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QY 1161 TTACGGAATTTGGCTAATACTTTTAAATGGTTAGAGGCTAATGGAACACGGGACCTGGT 1220
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LOCUS CQ868324 2145 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 25 from Patent WO2004074462.
ACCESSION CQ868324
VERSION CQ868324.1 GI:51998370
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 25 02-SEP-2004;
Athenix Corporation (US)
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Best Local Similarity 71.44; Pred. No. 3.2e-131;
Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;
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DB 68 ATAGAAAGACACCTGGCATATTTATTTAGGTGCTTTAAATAAAGACTATATAAGGAG 127
QY 169 TGAARAAGATGAGTCCATATCAAAATGAAATGAAATGAAATTTGGAAATCCTCATCGA 228
DB 128 TGAARAATATGAAATTTCTATCAAAATGAAATGAAATTTCTGGATGGTTCGCCGA 187
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QY 409 CACTATTATCAATAAGGAAACTAATTCGGACTAATCTGCTCAAACTGTGTCAGCACTTT 468
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QY 529 CGATTGCGAGATTTGACGGTAAATGAAATTTATAGAGATATATCTTTCTTATCTTCTG 588
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DB 548 AGAATGGCTTACG-----ATAATCAAACTCTAAATACTTGTGACG 592
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Search completed: December 19, 2005, 21:57:00
Job time : 19559.3 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	126.6	2.1	2711	9	BH771014	BH771014 LLMGtag73
2	77.6	1.3	471	10	CG807194	CG807194 1118078H0
C 3	75.8	1.3	1101	10	CNS0039G	AL063921 Drosophill
4	73.2	1.2	429	10	CG803197	CG803197 1118039H0
5	71.2	1.2	363	10	CG807311	CG807311 1118080F0
C 6	70	1.2	670	9	B3888480	B3888480 EIND421P
7	69.6	1.2	580	11	CR4799976	CR4799976 mth3-190L
C 8	69.6	1.2	685	10	CG957658	CG957658 MBEHE62TR
C 9	69.6	1.2	891	10	CG937914	CG937914 MBEHO73TR
10	68.6	1.1	379	10	CG807081	CG807081 1118077E0
11	68.2	1.1	832	9	BH391984	BH391984 AG-ND-138
12	68	1.1	735	10	CW960936	CW960936 A1AA-aac1
C 13	67.8	1.1	398	9	A2935561	A2935561 M028 E. c
14	67.6	1.1	302	10	CG807096	CG807096 1118077G0
15	67	1.1	679	4	AY066713	AY066713 Schmdtea
16	66.4	1.1	400	10	CG807323	CG807323 1118080G0
C 17	66.4	1.1	430	10	CG803196	CG803196 1118039H0
18	66.4	1.1	889	10	CW973509	CW973509 A1AA-aa5
C 19	66.2	1.1	518	10	CG086559	CG086559 PUJCQ11TD
C 20	66.2	1.1	891	10	CW952279	CW952279 Tcb38.1.B
C 21	65.6	1.1	707	10	CW187604	CW187604 104_607.1
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[illegible]

RESULT 2	CG807194	LOCUS	CG807194	471 bp	DNA	linear	GSS 10-NOV-2003
DEFINITION	1118078H01.Y1 1118	-	RescueMu Grid S	Zea mays	genomic	survey	sequence.

units. For more information on RescueMu, go to the web site 'www.zmbd.iastate.edu' and follow the links for 'RescueMu'. Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BstXI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN	Query Match	1.3%	Score 77.6;	DB 10;	Length 471;
	Best Local Similarity	52.1%;	Pred. No. 4.3e-06;		
	Matches 173;	Conservative 0;	Mismatches 159;	Indels 0;	Gaps 0;
Qy	3762	ATGATACAAATATACCTGCACACGGGTAAATATGTATGAGCAAAAGTTTAAATGGAAATT	3821		
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Qy	3822	ATAATCAAAATACCTAGCGATGCTGTTATACCACGGGTATACAAACAACATATAACCAAGACT	3881		
Db	192	ATAATAATAATTAATTTATAGTTTATTTATTAATTTATTAATTAATTAATTAATTAAT	251		
Qy	3882	CTAGTAATATGTATAATCAAAATTTATACTAACCAATGATGACCTGCATTCGGTTGCACAT	3941		
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Qy	3942	GTAACCAAGGCATACACTCTGGCTGTACATGTTAATCAAGGATATAACCGTTACGATTCT	4001		
Db	312	ATAATTAATAATTAATAATAATAATTTATAATAATAATAATTAATTAATAATAATAATAAT	371		
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Db	372	ATA	431		
Qy	4062	ATAACATAAGCTTTACAAATAAACGGACATATT	4093		
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RESULT 3
CNS0039G/c
LOCUS
DEFINITION
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
VERSION AL063921
KEYWORDS AL063921.1 GI:4941778
GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

FEATURES	source	Location/Qualifiers	COMMENT
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		/dev_stage="adult"	
		/lab_host="DH10B"	
		/clone_lib="1118 - RescueMu Grid S"	
		/note="Organ: leaf; Vector: RescueMu (engineered from pluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription	
			- web : www.genoscope.cns.fr/
			Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
(Access 1 to 425)
Walbot, M. Nonic sequences found using engineered Rescuemu transposon
Main published (2001)
Unpublished (2001)
Contact: walbot.v

Contact: Walbot V
Department of Biological Sciences

stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2327
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118039 row: 2
Class: transposon-tagged.
Location/Qualifiers
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/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from
pluscript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

	Query Match	1.2%; Score 73.2; DB 10; Length 429;	
	Best Local Similarity 51.6%; Pred. No. 4e-05;		
	Matches 191; Conservative 0; Mismatches 178; Indels 1; Gaps 1;		
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Dd	35	ATA	94
Qy	3822	ATAATCAAATACTAGCGATGTGTATTACCAAGGGTATACAAAACAACACTATAAACCAAGACT	3881
Dd	95	ATAATAATAAATTATTTATAATAATAATAATAATAATAATAATAATAATAATAATAATT	154
Qy	3882	CTAGTAATATGTATAATCAAAATTTACTTAACCAATCATGATGACCTTCGGTGGACAT	3941
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Dd	215	ATAATAATAATTTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA	274
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Dd	275	ATA	334
Qy	4061	CATAACATAAGCTTTACAAAATAACGGACATATTCTTAGAGAGGCTCCCTTAATTCATAAA	4120
Dd	335	ATA	394
Qy	4121	TAAGGAGATT 4130	
Dd	395	TAATTATAAT 404	

RESULT 4	
CG803197	
LOCUS	
DEFINITION	CG803197 429 bp DNA linear GSS 10-NOV-2003 1118039H04.yl 1118 - RescueMu Grid S Zea mays genomic, genomic survey sequence.
ACCESSION	
VERSION	CG803197
KEYWORDS	GSS.
SOURCE	CG803197.1 GI:382389B3
ORGANISM	Zea mays
	Zea mays

RESULT 5	
CG807311	
LOCUS	363 bp DNA linear GSS 10-NOV-2003
DEFINITION	1118080F01.v1 1118 - RescueMu Grid 5 Zea mays genomic, genomic survey sequence.
ACCESSION	CG807311
VERSION	CG807311.1 GI:38244939
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 363)
TITLE	Walbot, V.
JOURNAL	Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1118080 column: 3 Class: transposon-tagged.

FEATURES

FEATURES

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying logic and reasoning.	3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying logic and reasoning.
4. Robustness: The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.	4. Robustness: The model is highly resistant to adversarial attacks and data poisoning, ensuring reliable performance in real-world scenarios.
5. Efficiency: The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.	5. Efficiency: The model is optimized for fast inference and low resource consumption, making it ideal for deployment on edge devices.

ORIGIN

	Query Match	1.2%;	Score 71.2;	DB 10;	Length 363;
	Best Local Similarity	51.4%;	Pred. No. 0.00011;		
	Matches 163;	Conservative 0;	Mismatches 154;	Indels 0;	Gaps 0;
Qy	3718	TACATTTTATAGATACGATCGAGTTCCTTTGTATGCAAGGATATGATAACAAATAATAA	3777		
Db	47	TAATANTTTAATAATAATTTATATAATAATTTATATACTAATAAATTTATAATAATAATTTATAT	106		
Qy	3778	CCTGCACACGGGTAATATGTATGAGCAAGTTTAAATGGAATTTATTAATCAAATACTAG	3837		
Db	107	TTATAATTTACTCATTAATTTATAATAATAATTTATTAATTAATAATTTATAATTTATAA	166		
Qy	3838	CGATGTGTATTTACCAAGGGTATACAAACAACCTATAACCAAGACTCTAGTAAATATGTATAA	3897		
Db	167	TAATAATTTAATAATAATTAATTAATAATTTATAATAATAATTTATAATTAATTAATTAATAA	226		
Qy	3898	TCAAAAATTATACCTAAACATGATGACCTCGCATTCGGTTGCACATGTAAACCAAGGGCATAA	3957		
Db	227	TAATAAATTAATAATAATAGTTTATATAATAATTTATATAATAATTTATAATAATAATTAATCATAC	286		
Qy	3958	CTTCGGCTGTACATGTAATCAAGGATATAACCGTTTAACGATTCCTAAATATAGAATCAACAT	4017		
Db	287	TAATAAATTTAATAATAATAATAATAATAATTTATAATAATTTATAATAATAATAATAATAA	346		

Qy	4018	CATTGCGAAAAATAAAA	4034
Dd	347	TAATAATAATAATAATAA	363

RESULT 6	BZ388480/c	670 bp	DNA	linear	GSS 30-APR-2003
LOCUS	EINDL21tf	EI_10_12 KB	Entamoeba invadens	genomic clone	EINDL21,
DEFINITION	Genomic survey sequence.				
ACCESSION	BZ388480				
VERSION	BZ388480.1	GI:30235017			
KEYWORDS	GSS.				
SOURCE	Entamoeba invadens				
ORGANISM	Entamoeba invadens				
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.				
AUTHORS	Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van Dellen,K., Hall,N., Anderson,I. and Loftus,B.				
TITLE	Gene discovery in the Entamoeba invadens genome				
JOURNAL	Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)				
PUBMED	12798503				
COMMENT	Other GSSs: EINDL21tr				
	Contact: Brendan Loftus				
	Department of Eukaryotic Genomics				

[illegible]


```
ACCESSION CG937914
VERSION    CG937914.1 GI:39810051
KEYWORDS   GSS.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

REFERENCE  1 (bases 1 to 891)
            Town, C.D., Shetty, J., Koo, H. and Feldblum, T.F.
            Sequencing of BAC ends from Medicago truncatula
            Unpublished (2003)
            Other GSSs: MBEH073TF
            Contact: Chris Town
            TIGR

AUTHORS    7112 Medical Center Drive, Rockville, MD 20850, USA.
TITLE      Tel: 301-838-3523
JOURNAL    Fax: 301-838-0208
COMMENT    Email: cdtown@tigr.org
            Seq primer: CAGGAACAGCTATGACC
            Class: BAC ends.

FEATURES   Location/Qualifiers
            1..891
            /organism="Medicago truncatula"
            /mol_type="genomic DNA"
            /cultivar="genotype A17"
            /db_xref="taxon:3880"
            /clone="57N1"
            /clone_lib="mth2"
            /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
            HindIII; Cook, D.R. and Kim, D.J, unpublished"

ORIGIN
Query Match      1.2%; Score 69.6; DB 10; Length 891;
Best Local Similarity 50.6%; Pred. No. 0.00029; Indels 0; Gaps 0;
Matches 166; Conservative 0; Mismatches 164;

QY 3762 ATGATAACAATAATAACCTGCACACGGGTAATATGTATGAGCAAAAGTTTAAATGGAAT 3821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 508 ATAAGAATAATAAGNATAATAATAACAATAATAACAATAATAACAATAATAACAATA 449

QY 3822 ATAAATCAAAATACTACCGATGTGTATACCAAGGGTATACAACAACCTATAACCAAGACT 3881
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 448 ATAATAACAATAACAATAATAACAATAACAATAACAATAATAACAATAACAATAACA 389

QY 3882 CTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGCATTCGGGTGCACAT 3941
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 ATAATAACAATAACAATAATAACAATAACAATAACAATAATAATAATAACAATAACA 329

QY 3942 GTAACCAAGGGCATAACTCTGGCTGTACATGTAATCAAGGATATACCGTTAACGATTCT 4001
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 ATAACAATAACAATAACAATAATAACAACAATAACAATAATAACAATAACAATAATA 269

QY 4002 AAATAAGATCAACATCTTGGGAAAATAAABACCTACTACAAAATCTTGTGCATATC 4061
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 ACAATAACAATAACAATAACAATAACAATAACAATAACAATAACAATAACAATAATA 209

QY 4062 ATAACAATAAGCTTTACAATAAAGGACATATT 4093
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 ATAATAATAATAATAATAATAATAATAATAAT 177

RESULT 10
CG807081      379 bp DNA linear GSS 10-NOV-2003
LOCUS         1118077E02.y1.1118 - RescueMu Grid S Zea mays genomic, genomic
DEFINITION    survey sequence.
ACCESSION    CG807081
VERSION      CG807081.1 GI:38244576
KEYWORDS     Zea mays
SOURCE       Zea mays
ORGANISM     Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 379)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118077 column: 2
Class: transposon-tagged.

FEATURES   Location/Qualifiers
            1..379
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A188/B73"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="1118 - RescueMu Grid S"
            /note="Organ: leaf; Vector: RescueMu (engineered from
            pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
            RescueMu is a 4.9 kb, modified maize Mu transposon
            designed to allow plasmid rescue from total genomic DNA.
            Mu elements insert preferentially into transcription
            units. For more information on RescueMu, go to the web
            site 'www.zmdb.iastate.edu' and follow the links for
            'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
            extracted from leaf strips, double digested using BamHI
            and BglII, and ligated to form circular plasmids. DH10B
            cells were transformed and then screened on LB plates with
            ampicillin."

ORIGIN
Query Match      1.1%; Score 68.6; DB 10; Length 379;
Best Local Similarity 50.8%; Pred. No. 0.00042; Indels 0; Gaps 0;
Matches 164; Conservative 0; Mismatches 159;

QY 3761 TATGATAACAATAATAACCTGCACACGGGTAATATGTATGAGCAAAAGTTTAAATGGAAT 3820
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 TATATTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 115

QY 3821 TATAATCAAAATACTAGCGATGTGTATTACCAAGGGTATACAACAACCTATAACCAAGNC 3880
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 TATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 175

QY 3881 TCTAGTAATATGTATAATCAAAATTATACTAACAATGATGACCTGCATTCGGTTGCACA 3940
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 TATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 235

QY 3941 TGTAACCAAGGGCATAACTCTGGCTGTACATGTAATCAAGGATATACCGTTAACGATTC 4000
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 TATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 295

QY 4001 TAAATAAGAAATCAACATCATTCGCGAAAATAAABACCTACTACAAAATCTTGTGCATAT 4060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 TATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 355

QY 4061 CATACATAAGCTTTACAAATAA 4083
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 TATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 378

RESULT 11
BH391984
LOCUS         BH391984
DEFINITION    AG-ND-138G17.TR ND-TAM Anopheles gambiae genomic clone
```

AG-ND-138G17, genomic survey sequence.
 BH391984
 BH391984.1 GI:17338125
 GSS:
 Anopheles gambiae (African malaria mosquito)
 Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Culicidae; Anophelinae; Anopheles.
 1 (bases 1 to 832)
 Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
 Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
 Gardner,M.J. and Collins,F.H.
 Construction of a BAC library and generation of BAC end
 sequence-tagged connectors for genome sequencing of the African
 malaria mosquito Anopheles gambiae
 Mol. Genet. Genomics 268 (6), 720-728 (2003)
 12655398
 Other GSSs: AG-ND-138G17.TF.1
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: b.loftus@tigr.org
 This clone is from an A. gambiae BAC library (ND-TAM) provided by
 F.H. Collins and sequenced by The Institute for Genomic Research
 (TIGR). The BAC library was generated from A. gambiae PEST strain
 (DNA). All DNA was extracted from newly hatched first instar larvae
 to minimize the inclusion of DNA from microorganisms that inhabit
 the gut. The DNA is derived from mixed sexes of larvae. The BAC
 library was constructed at Texas A&M University BAC Center
 University, College Station, Texas 77843-2123, USA using a HindIII
 partial digest.
 Seq primer: M13 Rev
 Class: BAC ends.
 FEATURES
 source
 1. .832
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="PEST"
 /db_xref="taxon:7165"
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 /clone_lib="ND-TAM"
 /note="Vector: pECBAC1; Site_1: HindIII"
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 Best Local Similarity 50.1%; Pred. No. 0.00059;
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 QY 3747 TTGTATGCAAGATATGATAACAAATAATAAAGCTGGGTATATGTATGACAAA 3806
 DB 349 TTTATAATAATGATAATAATATTATATAATAATAATAATAATAATAATAATA 408
 QY 3807 GTTATAATGGAATTTATTAATCAAAATAGCATGTGTATACCAAGGTATACAA 3866
 DB 409 ATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 468
 QY 3867 ACTATAACCAAGACTCTAGTAATATGTATAATCAAAATATATCTAACAATGATGACTGC 3926
 DB 469 ATAATATTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 528
 QY 3927 ATTCCGGTTCACATGTAACCAAGGCGATAACTCTCGGCTGTACATGTAATCAAGGATATA 3986
 DB 529 ATAATGATAGTAAAAATCATATAATAATGATAATAATAATAATAAAAAAGATAATATAAT 588
 QY 3987 ACCGTTTAACGATTTCTAAATAAGAAATCAACATCATTCGCGAATAATAAACCTACTCACAA 4046
 DB 589 AATAATAATAATAAT -AATAATAGTAATAATAATAATAATAATAATAATAATAATA 647
 QY 4047 AATCTATTGCATATCATAACATAAGCTTTTACAATAACGACATATTCTTAGAAGAGGTCT 4106

DB 648 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 707
 QY 4107 CCTTAATTTCAAATAAGGAGATTTTTTT 4135
 DB 708 TATTATTATAATAATAATAATAAGATTTTT 736
 RESULT 12
 CW960936
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 CW960936.1 GI:56761663
 GSS:
 Ancylostoma caninum (dog hookworm)
 Ancylostoma caninum
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 Ancylostomatidae; Ancylostomatidae; Ancylostoma.
 1 (bases 1 to 735)
 Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagarishvili,R.,
 Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
 Waterston,R.H., Clifton,S.W. and Wilson,R.
 Genome Survey sequences from the parasitic nematode Ancylostoma
 caninum
 Unpublished (2004)
 Contact: Mitreva M
 Washington University in St. Louis
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: nematode@watson.wustl.edu
 Genomic DNA provided by John Hawdon (mtmjmh@wumc.edu) DNA
 sequenced by Washington University Genome Sequencing Center
 Class: shotgun.
 FEATURES
 Location/Qualifiers
 1. .735
 /organism="Ancylostoma caninum"
 /mol_type="genomic DNA"
 /strain="Baltimore"
 /db_xref="taxon:29170"
 /dev_stage="Adult"
 /lab_host="GS10"
 /clone_lib="Ancylostoma caninum whole genome shotgun
 library (AIAAGSS 001)"
 /note="Vector: pOTW13; Site 1: BstX1; Site 2: BstX1;
 Ancylostoma caninum genomic DNA was randomly sheared,
 end-repaired and size fractionated to enrich for 2-4 kb
 fragments. Genomic DNA was provided by John Hawdon
 (mtmjmh@wumc.edu) at George Washington University.
 Sequencing by Washington University Genome Sequencing
 Center, St. Louis, MO."
 ORIGIN
 Query Match 1.1%; Score 68; DB 10; Length 735;
 Best Local Similarity 50.3%; Pred. No. 0.00064;
 Matches 167; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
 QY 3762 ATGATAACAATAATAACCTGCACCGGTAATATGTATGACGAAAGTTATATGGAAT 3821
 DB 224 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 283
 QY 3822 ATAATCAAAATACTACGCGATGTATTACCAAGGGGTATACAACTACTAACCAAGACT 3881
 DB 284 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 343
 QY 3882 CTAGTAATAATGTATAATCAAAATTTACTAACAAATGATGACCTGCATCCGGTTGCACAT 3941
 DB 344 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 403
 QY 3942 GTAACCAAGGGCATAACTCTGCTGTACATGTAAATCAAGGATATACCGTTAACGATTCT 4001

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 09:48:39 ; Search time 2211.9 Seconds
(without alignments)
18019.361 Million cell updates/sec

Title: US-10-781-979-1

Perfect score: 5980

Sequence: 1 tacatgcaataacataaagag.....ttctaaaaagcctctgtat 5980

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5980	100.0	5980	13	ADR89400
2	2082	34.8	2082	13	ADR89401
3	2073	34.7	2073	13	ADR89403
4	1686	28.2	1686	13	ADR89405
5	967	16.2	4391	14	AEA61394
6	855	14.3	2145	13	ADR89413
7	790.6	13.2	3684	1	AAN82106
8	789	13.2	3684	6	ABK14949
9	789	13.2	3684	14	AEA61392
10	789	13.2	4085	1	AAN92515
11	787.4	13.2	3535	1	AAN91003
12	781.8	13.1	4184	1	AAN96139
13	774.6	13.0	4934	1	AAN81490
14	765.8	12.8	3543	2	AAQ81178
15	764.2	12.8	3543	2	AAQ14669
16	747.2	12.5	2019	13	ADR89414
17	739.8	12.4	2010	13	ADR89416
18	714	11.9	10974	1	AAN60055
19	639.8	10.7	4571	1	AAN93059
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					ADR89403 AXMI-008
					ADR89405 AXMI-008
					Aea61394 Bacillus
					ADR89413 AXMI-008
					Aan82106 Sequence
					Abk14949 Bacillus
					Aea61392 Bacillus
					Aan92515 Sequence
					Aan91003 Sequence
					Aan96139 Bacillus
					Aan81490 Insectici
					Aaql1178 B.t. toxi
					Aaql4669 Dipteran
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					ADR89416 AXMI-008
					Aan60055 VB131 clo
					Aan93059 Delta-end

20	450.6	7.5	3940	1	AAN93054	Delta-end
21	402	6.7	3756	1	AAN50525	Bacillus
22	390	6.5	4359	8	ABX13486	B. popill
23	390	6.5	4359	14	AE90814	Paenibaci
24	380.8	6.4	3690	6	ABK51132	cDNA enco
25	358	6.0	3797	2	AAQ36866	Coleopter
26	358	6.0	3797	2	AAQ58975	B.thuring
27	318.6	5.3	4366	8	ABX13497	B. popill
28	318.6	5.3	4366	14	AE90830	Paenibaci
29	317.8	5.3	3471	2	AAQ51704	Bacillus
30	314.6	5.3	3471	2	AAQ30821	Toxin 50C
31	314.6	5.3	3471	2	AAQ27167	Delta-end
32	314.6	5.3	3471	2	AAQ28940	B.thuring
33	314.6	5.3	3471	2	AAQ38653	Bt isolat
34	314.6	5.3	3471	2	AAQ38653	Bt isolat
35	313	5.2	4896	6	AAD43974	Antiscara
36	313	5.2	4896	10	ADF31301	Bacillus
37	313	5.2	4896	10	ADF31306	Bacillus
38	312.2	5.2	4359	8	ABX13496	B. popill
39	312.2	5.2	4359	14	AE90828	Paenibaci
40	310.4	5.2	6930	6	AAD43973	Bacillus
41	310.4	5.2	6930	10	ADF31299	Bacillus
42	310.4	5.2	6930	10	ADF31304	Bacillus
43	308.6	5.2	4004	2	AAQ05680	btPGS1245
44	308.2	5.2	4188	8	ABX13487	B. popill
45	308.2	5.2	4188	14	AE90816	Paenibaci

ALIGNMENTS

RESULT 1

ADR89400

ID ADR89400 standard; cDNA; 5980 BP.

XX AC ADR89400;

DT 18-NOV-2004 (first entry)

XX DE AXMI-008 full length coding sequence.

ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers

FT CDS 168..2249

FT /*tag= a

FT /product= "AXMI-008"

FT /transl_except= pos:168..170, aa:Met

XX WO2004074462-A2.

PN 02-SEP-2004.

PD 20-FEB-2004; 2004WO-US05829.

XX PR 20-FEB-2003; 2003US-0448632P.

PR 20-FEB-2003; 2003US-0448633P.

PR 20-FEB-2003; 2003US-0448806P.

PR 20-FEB-2003; 2003US-0448810P.

PR 20-FEB-2003; 2003US-0448812P.

PR 19-FEB-2004; 2004US-00781979.

PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.

PR 19-FEB-2004; 2004US-00782141.

PR 19-FEB-2004; 2004US-00782570.

PR 19-FEB-2004; 2004US-00783417.

XX

PA (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
XX P-PSDB; ADRB9402.
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX Claim 1; SEQ ID NO 12; 178pp; English.
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
XX endotoxin coding sequences of the invention have alternative start
XX codons, producing more than one protein from a single open reading frame.
XX The nucleic acid sequences of the invention are useful in DNA constructs
XX or expression cassettes for transformation and expression in plants and
XX bacteria. The nucleic acids and corresponding polypeptides are useful for
XX killing lepidopteran or coleopteran pests. Compositions containing the
XX delta-endotoxins of the invention, and methods for their production, are
XX useful for the production of organisms with pesticide resistance,
XX specifically bacteria and plants. These organisms are useful for
XX generating altered or improved delta-endotoxin or delta-endotoxin-
XX associated proteins that have pesticidal activity, or for detecting the
XX presence of delta-endotoxin or delta-endotoxin-associated proteins or
XX nucleic acids in products or organisms.
XX Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;
Query Match 100.0%; Score 5980; DB 13; Length 5980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACATGCAATACATAAGAGAGGTTTAAAAATCAATACCTCACCACAAAATTAATGGTT 60
DB 1 TACATGCAATACATAAGAGAGGTTTAAAAATCAATACCTCACCACAAAATTAATGGTT 60
QY 61 TATTGTGAGAAACATTGTTACAGGAATACATTCGGGTACTACGAATATATAGAAAGACAC 120
DB 61 TATTGTGAGAAACATTGTTACAGGAATACATTCGGGTACTACGAATATATAGAAAGACAC 120
QY 121 CTAACATATATTATTAGGTGCTTAAGATATAGGACTATATAGGAGTGAAGAAATGA 180
DB 121 CTAACATATATTATTAGGTGCTTAAGATATAGGACTATATAGGAGTGAAGAAATGA 180
QY 181 GTCATATCAAAATAAAATGAATATGAATATGGAACTCTCATCGAAATAACACAAATA 240
DB 181 GTCATATCAAAATAAAATGAATATGAATATGGAACTCTCATCGAAATAACACAAATA 240
QY 241 CGCCAAACAGATATCCTTTTGCAATAATCGGGATATGCTACTATGTCTTGGAAATGATT 300
DB 241 CGCCAAACAGATATCCTTTTGCAATAATCGGGATATGCTACTATGTCTTGGAAATGATT 300
QY 301 GTCAGGGAATCTCATGGGATGAATTTGGGAATCAGTCGAAACGATAACAGATTGGGA 360
DB 301 GTCAGGGAATCTCATGGGATGAATTTGGGAATCAGTCGAAACGATAACAGATTGGGA 360
QY 361 TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTATCAA 420
DB 361 TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTATCAA 420
QY 421 TAATAGGAAACATAATTCGACATAATCGTCAAACTGTGTGACGACCTTCTATATGATT 480
DB 421 TAATAGGAAACATAATTCGACATAATCGTCAAACTGTGTGACGACCTTCTATATGATT 480
QY 481 TATTATCTAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAGTGATGCGATTGCGAGATT 540
DB 481 TATTATCTAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAGTGATGCGATTGCGAGATT 540
QY 541 TTGACGGTAAATTTGAAAAATTTATAGAGGATTATCTTTCTTATCTTTGGGGCTTGGCTTA 600
DB 541 TTGACGGTAAATTTGAAAAATTTATAGAGGATTATCTTTCTTATCTTTGGGGCTTGGCTTA 600

QY 601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGACAAATTTAGTTATTATT 660
DB 601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGACAAATTTAGTTATTATT 660
QY 661 TTAAACTTTTCAGAAAGAGATTTCATGAAATTTCTAGGAGGGTCATTGTCAAGAAACAATG 720
DB 661 TTAAACTTTTCAGAAAGAGATTTCATGAAATTTCTAGGAGGGTCATTGTCAAGAAACAATG 720
QY 721 CTCAAGTATTGTTATTACCTACTTTTGACAAAGCTGCAAAATGTGAGTTATTACTATTAA 780
DB 721 CTCAAGTATTGTTATTACCTACTTTTGACAAAGCTGCAAAATGTGAGTTATTACTATTAA 780
QY 781 GGGATGCGAGTTCAATATATAAGCACAAATGGTTCCTATTTTGGTGTGAGTCAGAAATGTAAGAT 840
DB 781 GGGATGCGAGTTCAATATATAAGCACAAATGGTTCCTATTTTGGTGTGAGTCAGAAATGTAAGAT 840
QY 841 CGGAATTAATATACCTAACAGTGTGTTGATTTTACCGGTGATTACTATGAGCGGATTAA 900
DB 841 CGGAATTAATATACCTAACAGTGTGTTGATTTTACCGGTGATTACTATGAGCGGATTAA 900
QY 901 AATGCAAAACGGCAGAGTATACCAATTTATTGTTTATTTGGTGTATCAGGTAGGTTTAAATC 960
DB 901 AATGCAAAACGGCAGAGTATACCAATTTATTGTTTATTTGGTGTATCAGGTAGGTTTAAATC 960
QY 961 AGATAAAACAGGGGGGAGCAGGTGCTGACACTTGGTCGAAATTTAATAAATTTCTGTAGAG 1020
DB 961 AGATAAAACAGGGGGGAGCAGGTGCTGACACTTGGTCGAAATTTAATAAATTTCTGTAGAG 1020
QY 1021 AATGACGTTGGCGGTATTGGATATATCGCTATATTTCCAACTTATGATTTTGAGAAAT 1080
DB 1021 AATGACGTTGGCGGTATTGGATATATCGCTATATTTCCAACTTATGATTTTGAGAAAT 1080
QY 1081 ATCCATTTGCAACACATGTAGAGTTGACTAGGAAATTTATACAGATGCAAGTGGGATATT 1140
DB 1081 ATCCATTTGCAACACATGTAGAGTTGACTAGGAAATTTATACAGATGCAAGTGGGATATT 1140
QY 1141 CATCGGGAACCTTATAGTTGGTTACGGAATTTGGCCCTAACTTTTAAATGGGTTAGAGGCTA 1200
DB 1141 CATCGGGAACCTTATAGTTGGTTACGGAATTTGGCCCTAACTTTTAAATGGGTTAGAGGCTA 1200
QY 1201 ATGGAAACAGGGGACCTGGTTTGTAGTTACTTTGGCTTAGCAAAATAGTATATATATGAGT 1260
DB 1201 ATGGAAACAGGGGACCTGGTTTGTAGTTACTTTGGCTTAGCAAAATAGTATATATATGAGT 1260
QY 1261 ATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCATTATGAAGACTACACAAAG 1320
DB 1261 ATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCATTATGAAGACTACACAAAG 1320
QY 1321 GTAAACGGTATTTTCAACGATATGCTGGAACTACAGAGTAATGATCTACGTAATATTGATT 1380
DB 1321 GTAAACGGTATTTTCAACGATATGCTGGAACTACAGAGTAATGATCTACGTAATATTGATT 1380
QY 1381 TTCAAGATCCGATGTATATAAAATTTACTTTCAATAGCTATCATGAACCTAGTAGGAGAGA 1440
DB 1381 TTCAAGATCCGATGTATATAAAATTTACTTTCAATAGCTATCATGAACCTAGTAGGAGAGA 1440
QY 1441 CTACCGCTAGACAGAGTATCGTTTCAAAGCGAGATTTTCTGAGGGTAGGGGACCTG 1500
DB 1441 CTACCGCTAGACAGAGTATCGTTTCAAAGCGAGATTTTCTGAGGGTAGGGGACCTG 1500
QY 1501 ATTTAAATTTATGATGAGGTAATTAATGGCTAAGCGGATGACAAATTTGAATCTACGTTCC 1560
DB 1501 ATTTAAATTTATGATGAGGTAATTAATGGCTAAGCGGATGACAAATTTGAATCTACGTTCC 1560
QY 1561 CACTTGTATTGCACTCTAATGTTTGTAGAGGACCTCTCATAGATTATCAAAATGCGGCGAT 1620
DB 1561 CACTTGTATTGCACTCTAATGTTTGTAGAGGACCTCTCTCATAGATTATCAAAATGCGGCGAT 1620
QY 1621 GTGTTGTATATAGGAACTCCAGAGTTTAACTGATATGTTTGGACACATACAAGTTTAAAC 1680
DB 1621 GTGTTGTATATAGGAACTCCAGAGTTTAACTGATATGTTTGGACACATACAAGTTTAAAC 1680

QY 1681 GTGAAAATATATTTGAAGCCCAATCAAAATTAACAATAACCGCGGTGAAGATTATTAACC 1740
DB GTGAAAATATATTTGAAGCCCAATCAAAATTAACAATAACCGCGGTGAAGATTATTAACC 1740
QY 1741 TTCAAAATTTATCTTGTCTTAATGCTTATACCTATGTATTAATAAAGGCACATCATACAGGTGGG 1800
DB TTCAAAATTTATCTTGTCTTAATGCTTATACCTATGTATTAATAAAGGCACATCATACAGGTGGG 1800
QY 1801 ATTTAAATCCGTTTTTTAAGAACAAAATCAGAGTATACGAGTTTATGTCAGGTGGCGGAA 1860
DB ATTTAAATCCGTTTTTTAAGAACAAAATCAGAGTATACGAGTTTATGTCAGGTGGCGGAA 1860
QY 1861 TTAGATTGATTATTAATAACAAAATCGCAGACAAAAGTTTACCGTATTTTCGTTTATG 1920
DB TTAGATTGATTATTAATAACAAAATCGCAGACAAAAGTTTACCGTATTTTCGTTTATG 1920
QY 1921 CTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGTGGGGTTCAAAATC 1980
DB CTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGTGGGGTTCAAAATC 1980
QY 1981 GTTTTGTATCGCTTGAAAATCTTACTCTGAAAATTAATGACGATTTTAAATATAGTGATT 2040
DB GTTTTGTATCGCTTGAAAATCTTACTCTGAAAATTAATGACGATTTTAAATATAGTGATT 2040
QY 2041 TTAATTTTCGCTGAAATTTATCACACCTCCATTACCTAGTTCAACATTTAGATGCTGG 2100
DB TTAATTTTCGCTGAAATTTATCACACCTCCATTACCTAGTTCAACATTTAGATGCTGG 2100
QY 2101 AGATGCAAGCGAATAGTTTTCAATCAGATGTAAACGTGGTTCTCGACAAAATTTGAATTC 2160
DB AGATGCAAGCGAATAGTTTTCAATCAGATGTAAACGTGGTTCTCGACAAAATTTGAATTC 2160
QY 2161 TCCCAAGTATACAAACAATTTAGAAATATGAGGAGAACCGGACCTAGAAAACAAAGA 2220
DB TCCCAAGTATACAAACAATTTAGAAATATGAGGAGAACCGGACCTAGAAAACAAAGA 2220
QY 2221 ACGCGGTGAACGATCTGTTTTACCAATTTAAACAAAATAATTTACTAGAAATAGGTGATT 2280
DB ACGCGGTGAACGATCTGTTTTACCAATTTAAACAAAATAATTTACTAGAAATAGGTGATT 2280
QY 2281 GCTGTTTTAAACAATAAGCGAAAAGGTGTGAGTCTTATGTTTCAAGTAGTACGAAAAA 2340
DB GCTGTTTTAAACAATAAGCGAAAAGGTGTGAGTCTTATGTTTCAAGTAGTACGAAAAA 2340
QY 2341 TAGCTTAAAAATAGAAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATAGATG 2400
DB TAGCTTAAAAATAGAAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATAGATG 2400
QY 2401 TATGTCAGATGAACAAAATCCTCAGGAAAAATAATGTTATGGATGAAAATAAACTGGC 2460
DB TATGTCAGATGAACAAAATCCTCAGGAAAAATAATGTTATGGATGAAAATAAACTGGC 2460
QY 2461 AAAACAACCTTAGTCAGTCTCGTAACTCTACCTCCAAAATGGAGACTTTTCTGGGAATGTTG 2520
DB AAAACAACCTTAGTCAGTCTCGTAACTCTACCTCCAAAATGGAGACTTTTCTGGGAATGTTG 2520
QY 2521 GACATTCGGTAATGATATATAGGATCCCAATATCCTATTTTAAAGGAAAATTTCT 2580
DB GACATTCGGTAATGATATATAGGATCCCAATATCCTATTTTAAAGGAAAATTTCT 2580
QY 2581 ACAGATGCGTGGAGCAGACATATATGGAACCTCTATTTCCAACTTATCTGTCAAAA 2640
DB ACAGATGCGTGGAGCAGACATATATGGAACCTCTATTTCCAACTTATCTGTCAAAA 2640
QY 2641 AATAGATGAGTCTAAATTTAAAAACATATACAGTTATCGAGTAAGAGGTTTCTGGGAAG 2700
DB AATAGATGAGTCTAAATTTAAAAACATATACAGTTATCGAGTAAGAGGTTTCTGGGAAG 2700
QY 2701 TAGTAAAGATTTGAAATTAATGTATACACCTTACGGGAAGAAATTTGATGCTATCATGAA 2760
DB TAGTAAAGATTTGAAATTAATGTATACACCTTACGGGAAGAAATTTGATGCTATCATGAA 2760
QY 2761 TGTTCAAAATGATTTGGCCCTATATGAGCCCTAATCCTTCTATGTGGAGATTATCGCTGTGA 2820

DB TGTTCAAAATGATTTGGCCCTATATGAGCCCTAATCCTTCTATGTGGAGATTATCGCTGTGA 2820
QY 2821 ATCATCGTCTCAGTATGTGAGCCAAAGGTATCTTACACCAACAGATGGATATGCTCCCGA 2880
DB ATCATCGTCTCAGTATGTGAGCCAAAGGTATCTTACACCAACAGATGGATATGCTCCCGA 2880
QY 2881 TATGTATGATGATGCGCCCAAAATATAGTAAAGAGCATGTGAAGTGTACCATCGTCAATCC 2940
DB TATGTATGATGATGCGCCCAAAATATAGTAAAGAGCATGTGAAGTGTACCATCGTCAATCC 2940
QY 2941 ATTTTGAATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTTGATGT 3000
DB ATTTTGAATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTTGATGT 3000
QY 3001 CTTTATTTAAATTTCTAATTCAGATGATACGCTACAGTAGGGAATCTAGAAGTCAATTTGA 3060
DB CTTTATTTAAATTTCTAATTCAGATGATACGCTACAGTAGGGAATCTAGAAGTCAATTTGA 3060
QY 3061 AGAAGACCACTAACAGGTGAAGCATTTGGCACAATGTGAACAAAGGAAAGAAATCGAA 3120
DB AGAAGACCACTAACAGGTGAAGCATTTGGCACAATGTGAACAAAGGAAAGAAATCGAA 3120
QY 3121 ACAACATGCGGAGAAAAACGTTTGGGAAACAACAAGCCCTATGATCCAGCAAAAACAGGC 3180
DB ACAACATGCGGAGAAAAACGTTTGGGAAACAACAAGCCCTATGATCCAGCAAAAACAGGC 3180
QY 3181 TGTAGATGCAATTTTCAAAATGAACAGGTGTACACTATCATATTTACTTTAGATCATAT 3240
DB TGTAGATGCAATTTTCAAAATGAACAGGTGTACACTATCATATTTACTTTAGATCATAT 3240
QY 3241 TCAAAACGCTGATCGACTGCTACAGTCGATTCCTCTATGATACCAATTTGGTTTACCGAA 3300
DB TCAAAACGCTGATCGACTGCTACAGTCGATTCCTCTATGATACCAATTTGGTTTACCGAA 3300
QY 3301 TGTCTCCAGGTATGAACTATGATGTATATCAAGAGTTTAAACGCACTATCATGCAAGGTGA 3360
DB TGTCTCCAGGTATGAACTATGATGTATATCAAGAGTTTAAACGCACTATCATGCAAGGTGA 3360
QY 3361 TAATTTATATGATGACGAAAATGTCTATAACAAATGGTGTATTTACAAAGGATTTACAGG 3420
DB TAATTTATATGATGACGAAAATGTCTATAACAAATGGTGTATTTACAAAGGATTTACAGG 3420
QY 3421 ATGSCACGCAACAGGAAATGCGCGGTACAAACAAATGGATGGAGCTTCAGTATTTAGTTCT 3480
DB ATGSCACGCAACAGGAAATGCGCGGTACAAACAAATGGATGGAGCTTCAGTATTTAGTTCT 3480
QY 3481 ATCAAAATTTGAGCGCGGGGTATCTCAAAACTTTGCAATGCTCAAGATCATCATCGATATGT 3540
DB ATCAAAATTTGAGCGCGGGGTATCTCAAAACTTTGCAATGCTCAAGATCATCATCGATATGT 3540
QY 3541 GTTACGTGTGATTTGCCAAAAAAGAGGACCTGCGGAAAGGATGTGTAACGATGATGATTG 3600
DB GTTACGTGTGATTTGCCAAAAAAGAGGACCTGCGGAAAGGATGTGTAACGATGATGATTG 3600
QY 3601 TAATGGAAGAGCAAGAACTTAAGTTTCACTTTCTCGAAGAGGATATATGCAAAAAC 3660
DB TAATGGAAGAGCAAGAACTTAAGTTTCACTTTCTCGAAGAGGATATATGCAAAAAC 3660
QY 3661 AGTAGAGGTATTTCCCAAGAAAGTATCGTGTACGGATTGGAATAGGAGAAACCGAAGGTAC 3720
DB AGTAGAGGTATTTCCCAAGAAAGTATCGTGTACGGATTGGAATAGGAGAAACCGAAGGTAC 3720
QY 3721 ATTTTATATAGATGATCGAGTTGCTTTGTATGCAAGGATATGATAACAAATTAACCT 3780
DB ATTTTATATAGATGATCGAGTTGCTTTGTATGCAAGGATATGATAACAAATTAACCT 3780
QY 3781 GCACACGGTAAATGATGATGCAAGGATTTAATGGAATTTAATCMAAATCTAGCGA 3840
DB GCACACGGTAAATGATGATGCAAGGATTTAATGGAATTTAATCMAAATCTAGCGA 3840
QY 3841 TGTGTATTAACCAAGGATATACAAAACAACTATACCAAGACTCTAGTAAATGTATTAATCA 3900

XX AC ADR89401;
 XX DT 18-NOV-2004 (first entry)
 XX DE AXMI-008 coding sequence.
 XX KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
 KW expression cassette; transformation; transgenic; plant; bacteria;
 KW lepidoptera; coleoptera; pest; pesticide; resistance;
 KW pesticidal activity.
 XX OS *Bacillus thuringiensis*.
 XX FH Key Location/Qualifiers
 FT CDS 1..2082
 FT /*tag= a
 FT /product= "AXMI-008"
 FT /tranel_except= pos:1..3, aa:Met
 XX WO2004074462-A2.
 XX PN 02-SEP-2004.
 XX PD 20-FEB-2004; 2004WO-US005829.
 XX PF 20-FEB-2003; 2003US-0448632P.
 XX PR 20-FEB-2003; 2003US-0448633P.
 XX PR 20-FEB-2003; 2003US-0448797P.
 XX PR 20-FEB-2003; 2003US-0448806P.
 XX PR 20-FEB-2003; 2003US-0448810P.
 XX PR 20-FEB-2003; 2003US-0448812P.
 XX PR 19-FEB-2004; 2004US-00781979.
 XX PR 19-FEB-2004; 2004US-00782020.
 XX PR 13-FEB-2004; 2004US-00782096.
 XX PR 19-FEB-2004; 2004US-00782141.
 XX PR 19-FEB-2004; 2004US-00782570.
 XX PR 19-FEB-2004; 2004US-00783417.
 XX PA (ATHE-) ATHENIX CORP.
 XX PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX DR WPI; 2004-635574/61.
 XX DR P-PSDB; ADR89402.
 XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX PS Claim 1; SEQ ID NO 13; 178pp; English.
 XX CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX SQ Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;
 Query Match 34.8%; Score 2082; DB 13; Length 2082;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GTGAAAAGATGAGTCCATATCAAAATAAATAATGAAATATGAAATATTTGGAACTCTCATCG 227
 DB 1 GTGAAAAGATGAGTCCATATCAAAATAAATAATGAAATATGAAATATTTGGAACTCTCATCG 60
 QY 228 AATAACACAAATACGCCAAACAGATATCCTTTTGCAAATAATCGGATATGTCTACTATG 287
 DB 61 AATAACACAAATACGCCAAACAGATATCCTTTTGCAAATAATCGGATATGTCTACTATG 120
 QY 288 TCTTGGAAATGATGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA 347
 DB 121 TCTTGGAAATGATGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA 180
 QY 348 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 407
 DB 181 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240
 QY 408 ACATATATCAATAATAGGAAACCTAATTCGACCTAATCGTCAAACTGTGTGAGCACTT 467
 DB 241 ACATATATCAATAATAGGAAACCTAATTCGACCTAATCGTCAAACTGTGTGAGCACTT 300
 QY 468 TCTATATGTGATTTATTTATCTATATTCGTAAGAGGTAGCCGATAGTGTTTAAGTGAT 527
 DB 301 TCTATATGTGATTTATTTATCTATATTCGTAAGAGGTAGCCGATAGTGTTTAAGTGAT 360
 QY 528 GCGATTTGCAGATTTTGCACGTTAAATTTGAAAAATTTATAGAGAGTATTATCTTTCTTATCTT 587
 DB 361 GCGATTTGCAGATTTTGCACGTTAAATTTGAAAAATTTATAGAGAGTATTATCTTTCTTATCTT 420
 QY 588 GGGGCTTGGCTTAAAGACCGGTAAACCACTTCAAAAGACAAATAATTTCTGATATCGGACAA 647
 DB 421 GGGGCTTGGCTTAAAGACCGGTAAACCACTTCAAAAGACAAATAATTTCTGATATCGGACAA 480
 QY 648 TTAGTTTATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGAGAGGTCAATTG 707
 DB 481 TTAGTTTATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGAGAGGTCAATTG 540
 QY 708 TCAAGAAACAAATGCTCAAGTATTGTTTATACCTACTTTTGCACAAGCTGCAAAATGTGCAG 767
 DB 541 TCAAGAAACAAATGCTCAAGTATTGTTTATACCTACTTTTGCACAAGCTGCAAAATGTGCAG 600
 QY 768 TTATTAATAATTAAGGATGAGTTCAATATAAAGCAATGTTTCCATTTTGGAGTGCA 827
 DB 601 TTATTAATAATTAAGGATGAGTTCAATATAAAGCAATGTTTCCATTTTGGAGTGCA 660
 QY 828 GAGATGTAAGATCGGAATTAATATCACCCTAACAGTGGTGTGATTTTACCGGTGATTAC 887
 DB 661 GAGATGTAAGATCGGAATTAATATCACCCTAACAGTGGTGTGATTTTACCGGTGATTAC 720
 QY 888 TATGAGCGATTAATAATGCAAAACGCGAGAGTATACCAATTTATGTTTATATTCGATATCAG 947
 DB 721 TATGAGCGATTAATAATGCAAAACGCGAGAGTATACCAATTTATGTTTATATTCGATATCAG 780
 QY 948 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTTGGTGGAAATTAAT 1007
 DB 781 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTTGGTGGAAATTAAT 840
 QY 1008 AAATTTCTGAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCCACTTAT 1067
 DB 841 AAATTTCTGAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCCACTTAT 900
 QY 1068 GATTTTGGAGAAATATCCATTTGCCAACACATGTAGAGTTGACCTAGGGAATTTATACAGAT 1127
 DB 901 GATTTTGGAGAAATATCCATTTGCCAACACATGTAGAGTTGACCTAGGGAATTTATACAGAT 960
 QY 1128 GCAGTGGGATTTTCATCGGGAACTTATAGTTGGTTACCGGAATTTGGCTTAATTTAAT 1187
 DB 961 GCAGTGGGATTTTCATCGGGAACTTATAGTTGGTTACCGGAATTTGGCTTAATTTAAT 1020
 QY 1188 GGGTTAGAGGCTTAATGGAAACCGGGACCTGGTTAGTTTACTTGGCTTAGCAAAATAGGT 1247
 DB 1021 GGGTTAGAGGCTTAATGGAAACCGGGACCTGGTTAGTTTACTTGGCTTAGCAAAATAGGT 1080
 QY 1248 ATATATAATGAGTATGTTTTCGAGATATTTTTCGGCGCTGGTAGGAACCTCGTCATTATGAA 1307

Db 1081 ATATATAATAGATGTTTCGAGATATTTGCGCGCTGGGTAGGAATCTCGTATTATGAA 1140
QY GACTACAAAGGGTAACGGTATTTTCAACGATATCTCTGGAACTACGAGTATGATCTA 1367
Db 1141 GACTACAAAGGGTAACGGTATTTTCAACGATATCTCTGGAACTACGAGTATGATCTA 1200
QY CGTAATATTGATTTTCAGAAATGCGGATGATATATAAATAATCTTCAATAGCTATCATGAAC 1427
Db 1201 CGTAATATTGATTTTCAGAAATGCGGATGATATATAAATAATCTTCAATAGCTATCATGAAC 1260
QY CTAGTAGGAGAGACTACCGCTAGACAGAGATATCGTGTTCAAAGCAGATTTTCGTAGG 1487
Db 1261 CTAGTAGGAGAGACTACCGCTAGACAGAGATATCGTGTTCAAAGCAGATTTTCGTAGG 1320
QY GTAGGGGACCTGATTTAAATATATGATGACAGGTAATAATGCGGCTAAGCAGGATGACAAAT 1547
Db 1321 GTAGGGGACCTGATTTAAATATATGATGACAGGTAATAATGCGGCTAAGCAGGATGACAAAT 1380
QY GAATCTACGTTCCACTTGTATGCACTCTAATGCTGTAGAGACCTCTCATAGATTA 1607
Db 1381 GAATCTACGTTCCACTTGTATGCACTCTAATGCTGTAGAGACCTCTCATAGATTA 1440
QY TCAATGCGGCATGCTGTATATGCAAACTCCAGAGTTAAACGTATATGCTTGGACACAT 1667
Db 1441 TCAATGCGGCATGCTGTATATGCAAACTCCAGAGTTAAACGTATATGCTTGGACACAT 1500
QY ACAAGTTTAAACGTTGAAATATAATGAAAGCAATCAAAATACCAAAATACCGGCGGTG 1727
Db 1501 ACAAGTTTAAACGTTGAAATATAATGAAAGCAATCAAAATACCAAAATACCGGCGGTG 1560
QY AGAGATTATACCTTCAAAATATCTTGTGCTAATGCTTACCTATGCTATGCTATGCTATGCT 1787
Db 1561 AGAGATTATACCTTCAAAATATCTTGTGCTAATGCTTACCTATGCTATGCTATGCTATGCT 1620
QY CATACAGGTGGGATTTAATCCGTTTAAAGCAAAATCAGAGTATACCGAGTTTAT 1847
Db 1621 CATACAGGTGGGATTTAATCCGTTTAAAGCAAAATCAGAGTATACCGAGTTTAT 1680
QY GCAGGTGGCGGAATTAGATTGATTATTAATAACAAAGTTCACGAGTATACCGAGTTTAT 1907
Db 1681 GCAGGTGGCGGAATTAGATTGATTATTAATAACAAAGTTCACGAGTATACCGAGTTTAT 1740
QY CGTTTTCGTTATGCTCGAGATAAGCTGCTTCTTTAGTGTATATCTTTATCCAGAGGT 1967
Db 1741 CGTTTTCGTTATGCTCGAGATAAGCTGCTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
QY TGGGGTTCAAAATCGTTTGTATCGCTTGAAATCTTACTCTGGAATTTATGACGATTTA 2027
Db 1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAAATCTTACTCTGGAATTTATGACGATTTA 1860
QY AAATATAGTATGATTTTAAATTCGCTGAAATTTATCACACCTCCATTACCTAGTTCAAAAT 2087
Db 1861 AAATATAGTATGATTTTAAATTCGCTGAAATTTATCACACCTCCATTACCTAGTTCAAAAT 1920
QY CAGATGGATGAGAGATGCAAGCAATAGTTTTCATATCAGATGATAACGTTGTTCTCGAC 2147
Db 1921 CAGATGGATGAGAGATGCAAGCAATAGTTTTCATATCAGATGATAACGTTGTTCTCGAC 1980
QY AAAATTTGAATTCCTCCAGATATACAAACCTTTAGATATGAGGAGAACGGGACCTA 2207
Db 1981 AAAATTTGAATTCCTCCAGATATACAAACCTTTAGATATGAGGAGAACGGGACCTA 2040
QY GAAAAACAAAGAACCGGTGTAACGATCTGTTTACCAATTA 2249
Db 2041 GAAAAACAAAGAACCGGTGTAACGATCTGTTTACCAATTA 2082

RESULT 3
ADR89403
ID ADR89403
XX standard; cDNA; 2073 BP.
AC ADR89403;

XX 18-NOV-2004 (first entry)
XX AXMI-008 alternative start site coding sequence.
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX Bacillus thuringiensis.
XX Key Location/Qualifiers
FH 1..2073
FT /*tag= a
FT /product= "Alternative AXMI-008"
PN WO2004074462-A2.
XX 02-SEP-2004.
XX 20-FEB-2004; 2004WO-US005829.
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-0448797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 20-FEB-2003; 2003US-0448819P.
XX 20-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX WPI: 2004-635574/61.
XX P-PSDB; ADR89404.
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX Claim 1; SEQ ID NO 15; 178pp; English.
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
XX endotoxin coding sequences of the invention have alternative start
XX codons, producing more than one protein from a single open reading frame.
XX The nucleic acid sequences of the invention are useful in DNA constructs
XX or expression cassettes for transformation and expression in plants and
XX bacteria. The nucleic acids and corresponding polypeptides are useful for
XX killing lepidopteran or coleopteran pests. Compositions containing the
XX delta-endotoxins of the invention, and methods for their production, are
XX useful for the production of organisms with pesticide resistance,
XX specifically bacteria and plants. These organisms are useful for
XX generating altered or improved delta-endotoxin or delta-endotoxin-
XX associated proteins that have pesticidal activity, or for detecting the
XX presence of delta-endotoxin or delta-endotoxin-associated proteins or
XX nucleic acids in products or organisms.
XX Sequence 2073 BP; 694 A; 305 C; 431 G; 643 T; 0 U; 0 Other;
SQ Query Match 34.7%; Score 2073; DB 13; Length 2073;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 ATGAGTCCCATATCAAAATAAAAAATGAATATGAATATTCGAAATCCTCATCGAATAACACA 236
Db 1 ATGAGTCCCATATCAAAATAAAAAATGAATATGAATATTCGAAATCCTCATCGAATAACACA 60

DE	AXMI-008orf2 coding sequence.	
XX	ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;	
KW	expression cassette; transformation; transgenic; plant; bacteria;	
KW	lepidoptera; coleoptera; pest; pesticide; resistance;	
KW	pesticidal activity.	
XX		
OS	Bacillus thuringiensis.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1686
FT		/tag= a
FT		/product= "AXMI-008orf2"
FT		/transl_except= pos:1..3, aa:Met
XX	WO2004074462-A2.	
PN		
XX		
PD	02-SEP-2004.	
XX		
PF	20-FEB-2004; 2004WO-US005829.	
XX		
PR	20-FEB-2003; 2003US-0448632P.	
PR	20-FEB-2003; 2003US-0448633P.	
PR	20-FEB-2003; 2003US-0448797P.	
PR	20-FEB-2003; 2003US-0448806P.	
PR	20-FEB-2003; 2003US-0448810P.	
PR	20-FEB-2003; 2003US-0448812P.	
PR	19-FEB-2004; 2004US-00781979.	
PR	19-FEB-2004; 2004US-00782020.	
PR	19-FEB-2004; 2004US-00782096.	
PR	19-FEB-2004; 2004US-00782141.	
PR	19-FEB-2004; 2004US-00782570.	
PR	19-FEB-2004; 2004US-00783417.	
XX	(ATHE-) ATHENIX CORP.	
PA		
XX		
PI	Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;	
XX		
DR	WPI; 2004-635574/61.	
DR	P-PSDB; ADR89406.	
XX		
PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids	
PT	and polypeptides, useful for killing lepidopteran or coleopteran pests or	
PT	for producing organisms with pesticide resistance.	
XX		
XX	Claim 1; SEQ ID NO 17; 178pp; English.	
PS		
CC	This sequence encodes an isolated delta-endotoxin. Some of the delta-	
CC	endotoxin coding sequences of the invention have alternative start	
CC	codons, producing more than one protein from a single open reading frame.	
CC	The nucleic acid sequences of the invention are useful in DNA constructs	
CC	or expression cassettes for transformation and expression in plants and	
CC	bacteria. The nucleic acids and corresponding polypeptides are useful for	
CC	killing lepidopteran or coleopteran pests. Compositions containing the	
CC	delta-endotoxins of the invention, and methods for their production, are	
CC	useful for the production of organisms with pesticide resistance,	
CC	specifically bacteria and plants. These organisms are useful for	
CC	generating altered or improved delta-endotoxin or delta-endotoxin-	
CC	associated proteins that have pesticidal activity, or for detecting the	
CC	presence of delta-endotoxin or delta-endotoxin-associated proteins or	
CC	nucleic acids in products or organisms.	
XX		
SQ	Sequence 1686 BP; 624 A; 268 C; 348 G; 446 T; 0 U; 0 Other;	
	Query Match 28.2%; Score 1686; DB 13; Length 1686;	
	Best Local Similarity 100.0%; Pred. No. 2.8e-297;	
	Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2309 GTGAGTCTATGTTTACAGTAGTACGAAATAACGTTAAAAATAGAAACGACAGATTAT 2368	
Db		
	1 GTGAGTCTATGTTTACAGTAGTACGAAATAACGTTAAAAATAGAAACGACAGATTAT 60	
QY	2369 GAAATAGATCAAGCGCCATTTCTATAGATGTATGTCAGATGAACAAAATCCTCAGGAA 2428	

Db		61 GAAATAGATCAAGCGCCATTTCTATAGATGTATGTCAGATGAACAAAATCCTCAGGAA 120
QY		2429 AAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTA 2488
Db		121 AAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTA 180
QY		2489 CTCCAAAATGGAGACTTTTCTCGGAATGATTGGACATTCGGTAAATGATATTAATCATAGGA 2548
Db		181 CTCCAAAATGGAGACTTTTCTCGGAATGATTGGACATTCGGTAAATGATATTAATCATAGGA 240
QY		2549 TCCAATATCTCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGACAGACATATAT 2608
Db		241 TCCAATATCTCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGACAGACATATAT 300
QY		2609 GGAACTCTATTTCCAACTCTATCTGTCAAAAAATAGATGAGTCTAAAAATTAATAAACCATAT 2668
Db		301 GGAATCTCTATTTCCAACTCTATCTGTCAAAAAATAGATGAGTCTAAAAATTAATAAACCATAT 360
QY		2669 ACACGTTATCGAGTAAGAGGGTTTGTGGAAAGTAGTAAAGATTTGAAATTAATGTPAACA 2728
Db		361 ACACGTTATCGAGTAAGAGGGTTTGTGGAAAGTAGTAAAGATTTGAAATTAATGTPAACA 420
QY		2729 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCGAG 2788
Db		421 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCGAG 480
QY		2789 CCTAATCTCTCATGTGGAGATTTATCGCTGTGAATCATCGTCTCAGTATGTAGGCCCAAGGG 2848
Db		481 CCTAATCTCTCATGTGGAGATTTATCGCTGTGAATCATCGTCTCAGTATGTAGGCCCAAGGG 540
QY		2849 TATCTTACACCAACAGATGGATATGCTCCCGATATGTATGCGATGCCCGCAAAATATAGAT 2908
Db		541 TATCTTACACCAACAGATGGATATGCTCCCGATATGTATGCGATGCCCGCAAAATATAGAT 600
QY		2909 AGAAGAGCATGTGAAGTGTACCATGCTCATCCATTTGATTTTTCATATTCACACCGGAGAA 2968
Db		601 AGAAGAGCATGTGAAGTGTACCATGCTCATCCATTTGATTTTTCATATTCACACCGGAGAA 660
QY		2969 GTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGA 3028
Db		661 GTAGATACAAATACAAATGTAGGTATTGATGTCTTATTAAAAATTTCTAATCCAGATGGA 720
QY		3029 TACGCTACAGTAGGGAATCTAGAGTCAATTTGAAGAGGACCACTAACAGGTGAAGCATTTG 3088
Db		721 TACGCTACAGTAGGGAATCTAGAGTCAATTTGAAGAGGACCACTAACAGGTGAAGCATTTG 780
QY		3089 GCACATGTGAACAAAGGAAAGAAATGGAACCAACACATCGAGAGAAAACGTTGGGAA 3148
Db		781 GCACATGTGAACAAAGGAAAGAAATGGAACCAACACATCGAGAGAAAACGTTGGGAA 840
QY		3149 ACACAAAGCCCTATGATCCACAAAACAGGCTGTAGATGCAATTTATTACAAATGAACAA 3208
Db		841 ACACAAAGCCCTATGATCCACAAAACAGGCTGTAGATGCAATTTATTACAAATGAACAA 900
QY		3209 GAGTTACACTATCATATTACTTTTAGATCATATTTCAAAACGCTGATGCTGTTACAGTCG 3268
Db		901 GAGTTACACTATCATATTACTTTTAGATCATATTTCAAAACGCTGATGCTGTTACAGTCG 960
QY		3269 ATTCCCTATGTATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACCTATGATGTATAT 3328
Db		961 ATTCCCTATGTATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACCTATGATGTATAT 1020
QY		3329 CAAGAGTTAAACGCGCATCATGCAAGGTTTAAATTTATATATGATGACGAGAAATGTCATA 3388
Db		1021 CAAGAGTTAAACGCGCATCATGCAAGGTTTAAATTTATATATGATGACGAGAAATGTCATA 1080
QY		3389 ACAATGTTGACTTTTACCAAGGATTTACAGGATGCGACGCAACAGGAAATGCCGCGGTA 3448
Db		1081 ACAATGTTGACTTTTACCAAGGATTTACAGGATGCGACGCAACAGGAAATGCCGCGGTA 1140
QY		3449 CAACAAATGGATGGAGCTTTCAGTATTAGTTCTTATCAAAATTTGAGCGCGGGGTATCTCAA 3508


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QY 49 AAATAAATGGGTTATTTGTAGAAACATTTGTACAGGAATACATTTGGGTACTACGAATAT 108
DB 100 |||||
QY 8 AAATAAATGTTTTTTTGTAGAAACATTTGTACAGGAATACATTTGGGTACTACGAATAT 67
DB 100 |||||
QY 109 ATAGAAAGACACCTTAACATATATTTATAGTGTCCTTAATAAATAGGACTATATAAGGAG 168
DB 100 |||||
QY 68 ATAGAAAGACACCTGGCATATATTTATAGTGTCCTTAATAAATAGGACTATATAAGGAG 127
DB 100 |||||
QY 169 TGAATAAGATGAGTCCATATCAAAATAAATAAATGAATATGAATAATTCGATCCATCGA 228
DB 100 |||||
QY 128 TGAATAATAGATCTTATCAAAATAAATAAATGAATATGAATAATTCGATGTTCCCGGA 187
DB 100 |||||
QY 229 ATACACAAATACGCCAAACAGATATCCTTTTGCATAATATTCGGATATGTCTACTATGT 288
DB 100 |||||
QY 188 ATACACAAATATGTCAAACAGATATCCTTTTGCATAAAGGATCCAAATATATTCCTATTA 247
DB 100 |||||
QY 289 CTTCGAATGATGTCAGGAATCTCATGGATGAATAATTTGGGAATCAGTCGAACGATAA 348
DB 100 |||||
QY 248 ACCTGGACGCTTGTTCAGGGAAGGCCATGGCAAGATACGTCGGGAATCAGTCTCGGATATAG 307
DB 100 |||||
QY 349 CAAGTATTTGGGATAAATCTTATAGATTTTGTATAGAACCTAGTTCGGTGGGAATTAATA 408
DB 100 |||||
QY 308 TAACATATTTGGGACATACCTTATACAAATCTTGTCTAGAACCCGGTATAGGTGGGAATCCCTG 367
DB 100 |||||
QY 409 CACTATTTATCAATATAGGAAACTAATTCGACTAATTCGTCMAACTGTGTGACGACTTT 468
DB 100 |||||
QY 368 TAATATTTCAATAATAAACAACACTCAATTCGCTCTCTGTGTCATCTGTGGCAGCACTTT 427
DB 100 |||||
QY 469 CTATATGATTTATTTATCTATTAATTCGTAAGAGGTAGCGGATAGTGTGTTTTAAGTGATG 528
DB 100 |||||
QY 428 CTATATGATTTATTTAGTATCTATTAATTCGTAAGAGGTAGCGGATAGTGTGTTTTAAGTGATG 487
DB 100 |||||
QY 529 CGATTGACAGATTTTACGGTAAATTTGAAATAATATACAGATATTTATCTTTCTATCTTCG 588
DB 100 |||||
QY 488 GGGTTGACAGATTTTACGGTAAATTTGAAATAATATACAGATATTTATCTTTCTATCTTCG 547
DB 100 |||||
QY 589 GGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATATTTCTGATATCGGACAAT 648
DB 100 |||||
QY 548 AGGATTGGCTTACAG-----ATAAATCAATCTTAAATAAATCTGTGACG 592
DB 100 |||||
QY 649 TAGTTTATTTATTTAACTTTCAGAAAGAGATTTCAATGAAATCTTAGAGGGGTCAATGT 708
DB 100 |||||
QY 593 TAGTTAAACAGTTTCAAGACGCGGAAGAATTTCACTAAACTTTTAGCAGGGGTCAATTAT 652
DB 100 |||||
QY 709 CAAGAAACAATGCTCAAGTATGTTATTTACTACTTTTGCACAGCTGCAAAATGTCAGT 768
DB 100 |||||
QY 653 CAAGACAGAAGCTGGAATATTTATTTGCTTACGTATGTGCAAGCTGCAAAATGTCGATT 712
DB 100 |||||
QY 769 TATTACTATTTAAGGGATGCGAGTTCATATATAAAGCACAAATGTTTCCCAATTTTTCAGTGCAG 828
DB 100 |||||
QY 713 TATTACTATTTAAGGGACGCGAGTTAAATATATAAAGGAATCGGGACTAGTGTGTCACCGT 772
DB 100 |||||
QY 829 AGAATGTGAAGTCGAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTTACT 888
DB 100 |||||
QY 773 TGTATCCAGGTTCAGGGAGAA-----CTGATTGTA 802
DB 100 |||||
QY 889 ATGAGCGATTAAATATGAAAACGCGCAGATATACCAATTTATTTATATTTAGTATTCAGG 948
DB 100 |||||
QY 803 ACGAGCGGTTAAAGCGGAATAAAGAGATATACCAATTTATTTGTTAGGTGTTATTAACA 862
DB 100 |||||
QY 949 TAGGTTTAAATACAGATAAACAAGGGGGGACAGTGTCTGACACTTGTGCAAAATTTAATA 1008
DB 100 |||||
QY 863 AGGTTTATAGATCAGATAAAGACAGCGCGGTACAGTGTGAAATTTGTCGGAATTTAATA 922
DB 100 |||||
QY 1009 AATTTCTAGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTATG 1068
DB 100 |||||
QY 923 AATTTCTAGAGAAATGACGTTGGCGGTATTTGGATATTTATTTGCTATATTTTCCAACTTATG 982
DB 100 |||||
QY 1069 ATTTTGAGAAATATCCATTCGCAACATCTGAGATTGACTAGGGAATTTATACAGATG 1128
DB 100 |||||
QY 983 ATTTTGAAATATATCCATTTAGCAACAAGTGTAGAGTTTACTAGGGAAATTTATACAGATC 1042
DB 100 |||||
QY 1129 CAGTGGGATATTTATTCGGAACCTTATAGTTGGTTACGGAATTCGCTTAATACATTTTAAATG 1188
DB 100 |||||
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DB 1043 CAGTGGGATATTCAGGGGAAATTTATGTTGGGAACGGTTTT-----TTAGCTTTAATTT 1096
QY 1189 GGTTAGAGGCTAATGGAACACCGGGACCTCGTGTATTTAGTTACTTTGGCTTTAGCAAAATAGGTA 1248
DB 1097 CGGTAGAAGCAAAATGGAACACCGGGACCTCGTGTATTTAGTTACTTTGGCTTTCAAGCTATAGATA 1156
QY 1249 TATATATAGTATGATGTT-----TCGAGATATTTTTCGGGCTGGGTAGGAACTCGTC 1299
DB 1157 TATATAGTCAATCTTATTAATCTTCAGCTTGTATCTTTAGTGGCTGGGGGGAACTCGTC 1216
QY 1300 ATTATGAAGACTACACAAAGGGTAAACGGTATTTTCAACCGTATGTCTCGGAACCTACGAGTA 1359
DB 1217 ATTATGAAGACTTCACAAAGGGTAAACGGTCTTTTCAACCGTATGTCTCGGAACCTACGAGTA 1276
QY 1360 ATGATCTACGTAATATTTGATTTTCAGAAATGCCGATGTATATAAAATTTACTTTTATTAGCTA 1419
DB 1277 ATAATCCACGTAATATTTATTTTGGCAATACCGATATATTTAAATAATTTATTTTCAATTAGCTA 1336
QY 1420 TCATG---AACCTAGTAGGAGAGACTACCGCTAGACAGAGATATCGTGTGTTTCAAAAGGCAG 1476
DB 1337 GATATGCAATGCAACCGTTTTGTTGGGTATTTCAATCCACGGCATCTTTGTTTCAGCTGCAG 1396
QY 1477 ATTTTCGTAGGGTAGGGGACCTGATTTTAAATTTATGATGCAAGTAAATAATGGGCTAAAGCA 1536
DB 1397 AATTTTTCGCAACACACTAAATACTTTCTCTGTATGAGGTAAACAGTTCTTGGGTA---CT 1453
QY 1537 GGATGCAATTTGAATCTACGTTCCCACTGTGTATTTGCACTCTAA-----TGGTGTTAGAG 1590
DB 1454 CACAGACAAATTTGAATCTGTCTTACCAGGTATTAATAAGGATCTACCACTTAGTCGTACAA 1513
QY 1591 GACCTCTCATAGATTTATCAAAATGCGGCATGTGTGTATATGAAAATCCAGAGTTAAAG 1650
DB 1514 ATTACTCTCATAGATTTATCAAAATGCGGCATGTGTTCAAAATGAACCTCCAGAGTTAAAG 1573
QY 1651 TATATGTTTGGACACATACAAAGTTTAAACGCTGAAAATAATAATTGAAGCCAAATCAAAATTA 1710
DB 1574 TATTTGTTGGACACATACAGTATGAAAAGAGATTAATCGAATTTATCCAGATAAAATTA 1633
QY 1711 CACAAATACCGGGGTGAAGAGTTATTAACCTTCAAAATTTATCTTGTAAATGCTTATACCT 1770
DB 1634 CGCAAAATTCCTGAGTAAAGCTTTTGGCCCTACCAGAGGTACAGGATATGCAGGAGTT 1693
QY 1771 ATGTAATAAAGCACT 1787
DB 1694 ACCTCAGCTGGGCT 1710

RESULT 7
ID AAN82106 standard; DNA; 3684 BP.
XX
XX AAN82106;
XX AC
XX XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 13-NOV-1990 (first entry)
XX
DE Sequence contg. gene encoding Bacillus thuringiensis 8 protein.
XX Bt 8 protein; insecticides; mosquitoes; ss.
XX Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
RBS 145..149
FT /*tag= b
FT CDS 157..3567
FT /*tag= a
FT /*label= Bt 8 protein
XX
PN WO806631-A.
XX
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PD	07-SEP-1988.	
XX		
XX	03-MAR-1988; 88WO-US000734.	
XX		
XX	04-MAR-1987; 87US-00021405.	
PR		
XX	(UNMS) UNIV MICHIGAN STATE.	
PA	(PLAN-) PLANT GENETIC SYST.	
PA	(UNMI) UNIV MICHIGAN.	
XX		
XX	Vaeck MA, Chungjatup W, McIntosh L;	
PI		
XX	WFI; 1988-271170/38.	
DR	P-PSDB; AAP82314.	
XX		
PT	Chimeric gene for expression in Cyanobacteria - contg. DNA fragment	
PT	coding for insecticidal active protein produced by Bacillus strain.	
XX		
XX	Dioclosure; Page ?; 50pp; English.	
PS		
XX		
CC	This gene is ligated to a promoter region enabling expression in	
CC	Cyanobacteria and the resultant chimeric gene is used to produce Bacillus	
CC	thuringiensis 8 (Bt 8) protein. A truncated form of the protein can also	
CC	be produced using a shorter gene. Transformed cyanobacteria and their	
CC	progeny can be used in insecticidal compnsa., esp, for controlling	
CC	mosquitos. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on	
CC	25-MAR-2003 to correct PA field.)	
XX		
XX	Sequence 3684 BF; 1302 A; 585 C; 693 G; 1103 T; 0 U; 1 Other;	
SO		

Query Match	13.2%	Score 790.6;	DB 1;	Length 3684;
Best Local Similarity	71.4%	Pred. No. 2.7e-134;		
Matches 1093; Conservative	0;	Mismatches 414;	Indels 24;	Gaps 3;

2260	Qy	TTTACTAGAAATAGTGGTGTATGCTGTTTAAACAATAACGAAAGAGTTGTGAGTCCAT	2319
2064	Db	TGTATTAGATGAGACAGAGAACCAAAAATTTAGAAATCAGAACGAGAAATTTGTGAATGCAC	2123
2320	Qy	GTTTACAAGTAGTACGAAAATACGTTTAAAATATAGAAACGACAGATTATCGAATAGATCA	2379
2124	Db	GTTTACAAATGACCGGAAGATGCAATTAACAATTTGGAAACGACAGATTATGACATAGATCA	2183
2380	Qy	AGCGCCATTCTTATAGAAATGTATGTCCAGATGAACAAAATCCTCAGCAAAAAATAATGTT	2439
2184	Db	AGCGCAAACTCTCTGGAAATGCTATTTCTGAAGAAATATATCCAAAAGAAATGCTGTT	2243
2440	Qy	ATGGGATGAATAAATACTGGCAAAACAACTTAGTCAGTCTCGTAAATCTACTCCAAAATGG	2499
2244	Db	ATTAGATCAAGTTTAAAAATGCGAAACAACTTTAGTCAATCTCGAAATGTACTTCAAAACGG	2303
2500	Qy	AGACCTTT-----TCTCGGAATGATTCGACATTCGGTAAATGATATTATCATAGATCCAA	2553
2304	Db	GGATTTTGAATCGGCTACGCTTGGTGTGGACAAAGTGATAATATCAAAATTGAAGAAGA	2363
2554	Qy	TAATCTCTATTTTAAAGGAAAATTTCTACAGATCGTGGAGCAGACACATATATGGAAC	2613
2364	Db	TGATCTCTATTTTAAAGGGCATTAACCTTCATATCTCTGGGCGAGAGACATTGATGATAC	2423
2614	Qy	TCTATTTCCAACTATATCTGTCAAAAATAAGATGAGTCTAAATTTAAAAACATATACAG	2673
2424	Db	GATATTTCCGACCTATATATTTCCAAAAAATTTGATGAATCAAAATTA AAAACCGTATACAG	2483
2674	Qy	TTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGTGTACACGTTA	2733
2484	Db	TTACTCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTGAACCTAGTGGTTTCCACGCTA	2543
2734	Qy	CGGAAAAGAAATTGATGCTATCATCGAATGTTTCCAAATGATTGGCCTATATGTCAGCGCTAA	2793
2544	Db	TGGGGAAGAAATTCATGCCATCATGAATGTTCCAGCTGATTTAAACTATCTGTATCTTCTC	2603
2794	Qy	TCCTTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCGAGGGTATCC	2853
2604	Db	TAC-----CTTTGATTTGTGAAGGGTCTAAATCGTTTGTGAGACGTCGCGCTGTGCC	2651

RESULT 8
ABK14949
ID ABK14949 standard; DNA; 3684 BP.
XX
AC ABK14949;
XX
DT 29-AUG-2003 (revised)

08-MAY-2002 (first entry)

Bacillus thuringiensis variant israelensis toxin (Bt8) gene sequence.

Toxin; Bt8; insecticidal; cyanobacterium; synchocystis 680; endotoxin; mosquito control; glutamine synthetase inhibitor; inoculum; gene; ds.

Bacillus thuringiensis serovar israelensis.

Key Location/Qualifiers
RBS 145..149
/tag= a
/standard_name= "Shine-Dalgarno (SD) Sequence"
/note= "Consensus ribosome binding site"
CDS 157..3567
/*tag= b
/product= "Bacillus thuringiensis toxin (Bt8) protein"
/transl_except= (pos:1708..1710, aa:Ser)
/transl_except= (pos:2356..2358, aa:Gln)
/transl_except= (pos:3067..3069, aa:Gln)

US6335008-B1.

01-JAN-2002.

18-FEB-1992; 92US-00837625.

04-MAR-1987; 87US-00021405.

13-SEP-1988; 88US-00243798.

(UNMS) UNIV MICHIGAN STATE.

Vaeck MA, Chungjatupornchai W, McIntosh L;
WPI; 2002-163196/21.
P-PSDB; AAU76029.

Novel chimeric gene expressed in cells of Cyanobacterium for controlling mosquitoes in water, comprises a DNA fragment comprising promoter region and a DNA fragment containing gene encoding for insecticidal protein.

Example 2; Fig 2a; 36pp; English.

The present invention relates to a new chimeric gene expressed in cells of a Cyanobacterium such as Synchocystis 680. The gene comprises a DNA fragment having a promoter region, for expression of a DNA fragment in the Cyanobacterium, and a fragment coding for an insecticidally active protein endotoxin produced by Bacillus thuringiensis, B. sphaericus or B. kurstaki strain, or for a truncated form of the protein. Cyanobacterium is useful for controlling mosquitoes in water by applying the bacterium to a region to be controlled, where the cyanobacterium which contain and express the bar gene are selectively protected against competing non-transformed Cyanobacteria by treating the region with glutamine synthetase inhibitors. The invention is useful as viable inoculum to settle the regions, especially the swamps and all stagnant waters/ which promote the growth of mosquito larvae. Cyanobacterium provides better control of mosquitoes, ensures a long-term destruction of mosquitoes, guarantees direct uptake of the bacterium by the mosquitoes and assures more stable availability of the toxin in the vicinity surface since it is self replicating and floats at or near the water surface. The present nucleic acid sequence encodes the B. thuringiensis variant israelensis toxin (Bt8) protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 3684 BP; 1301 A; 587 C; 694 G; 1102 T; 0 U; 0 Other;

Query Match 13.2%; Score 789; DB 6; Length 3684;
Best Local Similarity 71.3%; Pred. No. 5.2e-134;
Matches 1092; Conservative 0; Mismatches 415; Indels 24; Gaps 3;

QY 2260 TTCTACTAGATAGGTGTTGCTGTTTAAACAAATTAAGCGAAAGGTTGTGAGTCCTAT 2319
DB 2064 TGTATTAGATGACACAGAGAACCAAAATTTAGAAATCAGAACGAGAGTTGTGAATGCACT 2123

QY 2320 GTTTACAAGTAGTACGAAATAACGTTAAATAATAGAAACGACAGATTATGAAATAGTCA 2379
DB 2124 GTTTACAATAGCGCGAAAGATGCAATTAACATTTGGAACGACAGATTATGACATAGATCA 2183
QY 2380 AGCGGCCATTTCTATAGAATGTATGTAGATGAACAAAATCCCTCAGGAAAAAATAATGTT 2439
DB 2184 AGCGCGAAATCTTGTGGAATGATTTCTGAAGAATTTATATCAAAAAGAAAATGCTGTT 2243
QY 2440 ATGGGATGAATTAATAACTGGCAAAACAACTTAGTCTAGTCTCGTAATCTACTCCAAATGG 2499
DB 2244 ATTAGATGAAGTTAAATAATGCGAAACAACTTAGTCTAGTCTCGAAATGTACTTCAAAACGG 2303
QY 2500 AGACTTTT-----TCTGGGAAATGATTGGACATTTCCGCTAATGATTAATATCATAGATCCAA 2553
DB 2304 GGAATTTGAATCGGCTACGCTTGGTTGGACAACAGTGAATATATCACAATTTGAAGAGA 2363
QY 2554 TAATCCTATTTTAAAGGAAAAATTTCTACAGATGCGTGGAGCAGCAGACATATATGGAAC 2613
DB 2364 TGATCCTATTTTAAAGGCAATTTACCTTCATATGCTCTGGGCGAGAGACATTTGATGTTAC 2423
QY 2614 TCTATTTCCAACTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAACCATATATACAG 2673
DB 2424 GATATTTCCGACCTATATATTTCCAAAAAATTTGATGAATCAAAATTTAAACCGTATACACG 2483
QY 2674 TTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAGGATTTGAAATTAATGTAACACGTTA 2733
DB 2484 TTACCTAGTAGGGGATTTGTAGGAAGTAGTAAGAGTAGTAAGACTAGTGGTTTTCACGCTA 2543
QY 2734 CGGGAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTTGGCCTATATGACAGCTTA 2793
DB 2544 TGGGGAAGAAATTTGATGCTATCATGAATGTTCCAGCTGATTTAAACTATCTGATCCTTC 2603
QY 2794 TCTTTCATGTGGAGATTTCGGCTGTGAATCATGCTCTAGTATGTGAGCCAAAGGGTATCC 2853
DB 2604 TAC-----CTTTGATTTGTGAAGGGTCTAATCGTTGTGAGACGCTCCGCTGTGCC 2651
QY 2854 TACACCAACAGATGGATATGCTCCCGATATGATGCATGCTCCCGCAAAATATAGATAGAA 2913
DB 2652 GGTAAACATGGGAACACTTCTGATATGTTGTTATTCATGCCAATATGATACAGGGAATA 2711
QY 2914 GCATGTGAAGTGTACGATCGTCATCCATTTGATTTTTCATATTTGACACCGGAGAACTAGA 2973
DB 2712 GCATGTGCTATGTGAGATTCCCATCAATTTAGTTTCACTATTTGATACAGGGGCATTAGA 2771
QY 2974 TACAATACAATGTAGTATTTGATGCTCTTATTAATAATTTCTAATTCAGATGGATACGC 3033
DB 2772 TACAATGAAAAATATAGGGGTTTGGGTCATGTTTAAATATCTTCTCCAGATGGATACGC 2831
QY 3034 TACAGTAGGGAATCTAGAGTCAATTGAAGAAGGCCACTAACACAGGTGAAGCATTTGGCACA 3093
DB 2832 ATCATTAGATAATTTAGAAAGTAAATTTGAAGAAGGCCAATAGATGGGGAAGCACTGTACG 2891
QY 3094 TGTGAAACAAAAAGGAAAAAATGGAACAACACATGGAGAAAAAATCGTTGGGAAAAACACA 3153
DB 2892 CGTGAACACACATGGAGAAATGGAACCATCAATTTGAAGCAAAACGTTCCGAAAAACACA 2951
QY 3154 ACAAGCTATGATCCAGCAAAAACAGGCTGTAGATGCAATTTATTAACAATTTGAACAAGA--- 3210
DB 2952 ACAAGCATATGATGTAGCGAAAAACAAGCCATTGATGCTTTTATTCACAAAATGTACAAGATGA 3011
QY 3211 ---GTTACACTATCATATTTACTTTTAGATCATATTCAAAACGGTGTGACTCGACTGACAGTC 3267
DB 3012 GGGTTTACAGTTTGATACACACTCGCTCAAAATTCAGTACGCTGAGTATTTGGTACCATC 3071
QY 3268 GATTCCTATGTATACATAATTTGGTTTACCAGATGCTCCAGGTATGAACTATGATGTATA 3327
DB 3072 GATTCATATGTACAAATGATTTGGTTGTCAGATGTTCCAGGTATGAATTTATGATATCTA 3131
QY 3328 TCAAGATTAAACGACCGTATCATGCAAGGTTTAAATTTATATGATGACGAAATGTCAT 3387
DB 3132 TGTAGAGTTGGATGACAGAGTGGCACAGCGGGTTATTTGTTATGATACAAAGAAATATTAT 3191

QY 3388 AACAAATGGTGACTTTACACAGGATTACAGGATGGCAGCGAACAGGAAATGCCCGGT 3447
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3192 TAAAAATGGTGATTTTACACAGGGGTAATGGGGTGGCATGTAACTGGAAATGCAGACGT 3251
 QY 3448 ACAACAAATGGATGGAGCTTCAGTATTAGTCTCATCAAAATGGAGCGCGGGGTACTCA 3507
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3252 ACACAAATAGATGGGTGTTCTGTATTGGTTCATCTAAATGGAGTGGCTGGCGTATCTCA 3311
 QY 3508 AAACCTTGCATGCTCAAGATCATCATGATATGTTTACGTGTGATTGCCAAAGGAGG 3567
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3312 AAATGTCATCTCCAACATAATCATGGTATGCTTACGTGTTATTGGCCAAAAGAGG 3371
 QY 3568 ACTGGAAGAGGTATGTAAACGATGATGGAATGTAATGGAAGCAGAGAAACACTTAAGTT 3627
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3372 ACCTGGAATGGGTATGTCAACGCTTATGGATTGTGAGGAGAAATCAAGAAAAATTCACGTT 3431
 QY 3628 CACTCTCTCGAAGAGGATATATGACAAAACAGTAGAGGTATTTCCAGAAAGTATCG 3687
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3432 TAGCTCTTGGAAGAGGATATATTACGAAGACAGTAGATGTATTCCAGATACAGATCG 3491
 QY 3688 TGTACGGATTGAAATAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCT 3747
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3492 TGTACGAATGTAGATAGGCGAAACCGAGGTTGTTTTATATCGAAAGCATTTGAATTAT 3551
 QY 3748 TTGTATGCAAGGATATGATAACAATTAATAC 3778
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 3552 TTGCATGAACGAGTGATTAAATAAAAAATAAC 3582

RESULT 9

AEA61392
 ID AEA61392 standard; DNA; 3684 BP.
 XX
 AC AEA61392;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Bacillus thuringiensis Cry4Ba coding sequence, SEQ ID 2.
 XX
 KW Insecticide; crystal protein; Cry4Ba; gene; ds.
 XX
 OS Bacillus thuringiensis.

Key Location/Qualifiers
 CDS 157..3567
 FT /*tag= a
 FT /product= "Cry4Ba"
 FT

US2005124803-A1.

09-JUN-2005.

30-AUG-2004; 2004US-00929754.

29-AUG-2003; 2003US-0498826P.

(OHIS) UNIV OHIO STATE RES FOUND.

Dean DH, Abdullah MA;

WPI; 2005-417057/42.

P-PSDB; AEA61391.

EMBL; X07423.

PT New modified Bacillus thuringiensis insecticidal crystal proteins (i.e. Cry4Ba and Cry19a) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.

XX Disclosure; SEQ ID NO 2; 63pp; English.

PS The present invention relates to modified insecticidal Bacillus

CC thuringiensis crystal proteins Cry4Ba and Cry19a which have enhanced

CC toxicity against a variety of insects, e.g. mosquitoes and lepidoptera.
 CC The modified proteins are useful for reducing or eliminating populations
 CC of target insects that are vectors of disease, particularly mosquitoes.
 CC The present sequence is the coding sequence for the wild-type Cry4Ba
 CC protein, which can be modified as follows: the amino acid aspartic acid
 CC at position 454 is substituted with, for example proline, glycine,
 CC alanine or threonine, and at least two or more additional amino acids are
 CC inserted after the substitution, where the amino acids inserted after the
 CC substituted amino acid at position 454 are selected from the combinations
 CC of alanine and threonine or alanine and valine. In addition, the modified
 CC Cry4Ba protein may comprise the following substitutions: Thr456 is
 CC replaced with Ala; Asn578 is replaced with alanine; Asn579 is replaced
 CC with alanine; Ile580 is replaced with alanine, phenylalanine or tyrosine;
 CC Ile581 is replaced with alanine or phenylalanine.
 XX

SQ Sequence 3684 BP; 1302 A; 587 C; 692 G; 1103 T; 0 U; 0 Other;

Query Match 13.2%; Score 789; DB 14; Length 3684;
 Best Local Similarity 71.3%; Pred. No. 5.2e-134;
 Matches 1092; Conservative 0; Mismatches 415; Indels 24; Gaps 3;

QY 2260 TTTACTAGAAATAGGTGGTATTGCTGTTTAAACAAATAAGCGAAAAAGGTTGTGAGTCCTAT 2319
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2064 TGTATTAGTAGACAGAGAACCAAAATTTAGAAATCAGAACGAGAAGTTGTGAATGCAT 2123
 QY 2320 GTTTACAAAGTAGTACGNAAAAATACGTTAAAAATAGAAAACGACAGATTATGAAATAGATCA 2379
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2124 GTTTACAAATGACGCGAAAGATGCATTTAAACATTTGGAACGACAGATTATGACATAGATCA 2183
 QY 2380 AGCGGCCATTTCTATAGAAATGTATGTCAGATGAAACAAATCTCAGGAAAAAATATGTT 2439
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2184 AGCCGCAAAATCTTGTGGAATGTATTCTGAAGAAATTTATATCCAAAAGAAAAAATGCTGT 2243
 QY 2440 ATGGGATGAATAAATAAATCTGGCAAAACAACTTAGTCAGTCTCGTAATCTACTCAAAATGG 2499
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2244 ATTAGATGAAGTTAAAAATGCGAAACAACTTAGTCAATCTCGAAATGTACTTTCAAAACGG 2303
 QY 2500 AGACTTT-----TCGGGAATGATTGGACATTCGGTAATGATATATCATAGGATCCAA 2553
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2304 GGATTTTGAATCGGCTACGCTTGGTTGGACAAAGTGTATAATATCACAATTTCAAGAAAGA 2363
 QY 2554 TAATCCTATTTTAAAGGAAAAATTTCTACAGATGCGTGGAGCAGCAGACATATATGGAC 2613
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2364 TGATCCTATTTTAAAGGGGCATTACCTTCATATGTCTGGGGCGAGAGACATTTGATGGTAC 2423
 QY 2614 TCTATTTCCAACCTATATCTGTCAAAAAATAGATCAGTCTAAATTTAAACCAATATACACG 2673
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2424 GATATTTCCGACCTATATATTTCCAAAAAATTTGATGAATCAAAATTTAAAACCGTATACAG 2483
 QY 2674 TTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTTAAATGGTTAACAGTTA 2733
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2484 TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAAGATGTAGAACTAGTGGTTTTCACGCTA 2543
 QY 2734 CGGGAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATACAGCCTAA 2793
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2544 TCGGGAAGAAATTTGATGCCATCATGAATGTTCCAGCTGATTTTAAACTATCTGTATCCTTC 2603
 QY 2794 TCCTTTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCC 2853
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2604 TAC-----CTTTGATTGTGAAGGGTCTAATCGTTGTGAGACGTCGCTGTGCC 2651
 QY 2854 TACACCAACAGATGGATATGCTCCCGATATGATGATGATGCCCGCAAAATATATAGATAGAAA 2913
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2652 GGCTAACATTTGGGAACACATCTCTGATATGTTGTTATTTTCATGCCCAATATGATACAGGAAAA 2711
 QY 2914 GCATGTGAAGTGTACAGATCGTCATCCATTTGATTTTCATATTTGACACCGGAGAGATAGA 2973
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2712 GCATGTGCTATGTCCAGGATTCCTCAATTTAGTTTCACTATGATACAGGGGCATTAGA 2771
 QY 2974 TACAAATACAAATGTAGGTATTGATGTCCTTATTAAAAAATTTCTAATCCAGATGGATACGC 3033
 DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 DB 2772 TACAAATGAAATATAGGGGTTGGTTCATGTTTAAATATCTTCTCCAGATGGATACGC 2831

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QY 3034 TACAGTAGGAATCTAGAGTCATTGAAGAGGACCACTAACGGTGAAGCATTTGGCACA 3093
DB |||||
QY 2832 ATCAATAGATAATTTAGAGTAATTTGAAGAGGSCCAATAGATGGGGAAGCACTGTCAAG 2891
DB |||||
QY 3094 TGTGAACAAAGGAAAGAAATGGAAACACACATGGAGAAAACGTTGGGAAACACA 3153
DB |||||
QY 2892 CGTGAACACATGGAGAGAAATGGAAACGATCAATGGAGCAAAACGTTTCGGAACACA 2951
DB |||||
QY 3154 ACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTTTACAAATGAACAAGA-- 3210
DB |||||
QY 2952 ACAAGCATATGATGTAGCGAAACAGGCCATTTGCTTTTATTCACAAATGTACAAGATGA 3011
DB |||||
QY 3211 ---GTTACATATCATATTACTTTAGATCATATTTCAAACGCTGATCGACTGGTACAGTC 3267
DB |||||
QY 3012 GGGCTTTACAGTTTGATACGACACTCGCTCAAAATTCAGTACGCTGAGTATTTGGTACAATC 3071
DB |||||
QY 3268 GATTCCCTATGTATACCAATATTTGGTTTACGAATGCTCCAGGTATGAACTATGATGTATA 3327
DB |||||
QY 3072 GATTCCCATATGTGTACAAATGATTTGGTTGTGATGATGTTCCAGGTATGAATTTATGATCTA 3131
DB |||||
QY 3328 TCAAGAGTTAAACGACGCTATCATGCAAGGTTTATAATTTATATGATGCACGAAATGTCAT 3387
DB |||||
QY 3132 TGTAGAGTTGGATGTCAGAGTGGCAACAGCGGTTATTTGATGATACAAAGAAATATAT 3191
DB |||||
QY 3388 AACAAATGGTGACTTTTACAAAGGATTTACAGGATGGCACGCAACAGGAAATGCCGCGT 3447
DB |||||
QY 3192 TAAAAATGGTGATTTTACAAAGGGGTAATGGGTTGCGATGTAACCTGGAATGCAGACGT 3251
DB |||||
QY 3448 ACAACAAATCGATGGAGCTTCAGTATTTAGTTTCTATCAAAATTTGAGCGCGGGGTATCTCA 3507
DB |||||
QY 3252 ACAACAAATAGATGGTGTTTCTGTATTTGGTTCTATCTAATTTGGAGTGCTGGCGTATCTCA 3311
DB |||||
QY 3508 AAACCTTGATGCTCAAGATCATGATGATGTTTACGTTGATGTTCCCAAAAGGAGG 3567
DB |||||
QY 3312 AAATGTCCTCTCAACATTAATCATGGTATGCTTACGTTGTTATTCGCAAAAGGAGG 3371
DB |||||
QY 3568 ACCTGGAAGAGGATGTATACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTT 3627
DB |||||
QY 3372 ACCTGGAATGGGTATGTCTACGCTTATGGATTGTGAGGAGAAATCAAGAAATTTGACGTT 3431
DB |||||
QY 3628 CACTTCTTGGAAGAGGATATATGACAAACAGATAGAGGTATTTCCGAAAGATGATCG 3687
DB |||||
QY 3432 TAGCTCTTGGAAGAGGATATATACGAAAGACAGTATGATTTTCCAGATACAGATCG 3491
DB |||||
QY 3688 TGTACGGATTTGAATAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCCAGTTGCT 3747
DB |||||
QY 3492 TGTACGAAATTTGATAGGCGGAAACCGAAGGTTTCGTTTATATATCGAAAGCATTTGAATTAAT 3551
DB |||||
QY 3748 TTGTATGCAAGGATATGATTAACAAATAATAC 3778
DB |||||
QY 3552 TTGCATGAACGAGTGATTATTAATAATAATAAC 3582
DB |||||
```

RESULT 10

AAN92515

ID AAN92515 standard; DNA; 4065 BP.

XX AC

XX AC

XX AC

DT 25-MAR-2003 (revised)

DT 23-DEC-1990 (revised)

DT 15-MAY-1990 (first entry)

XX XX

XX XX

DE Sequence of insecticide gene from *Bacillus thuringiensis israelensis*

DE strain.

XX XX

XX XX

OS *Bacillus thuringiensis*.

XX XX

FH Key Location/Qualifiers

FT CDS 461..3868

/*tag= a

```
XX JP01080294-A.
PN XX
XX 27-MAR-1989.
PD XX
XX 21-SEP-1987; 87JP-00238394.
XX 21-SEP-1987; 87JP-00238394.
XX 21-SEP-1987; 87JP-00238394.
XX (SUMO) SUMITOMO CHEM IND KK.
XX (MARU-) MARUBENI KK.
XX WPI; 1989-134798/18.
XX P-PSDB; AAP93308.
XX Insecticide protein gene - from Bacillus thuringiensis israelensis
XX strain, used to produce protein toxic to diptera larvae, eg. aedes.
XX Fig 2; Fig 2-1 to 2-3; 8pp; Japanese.
XX The protein gene has high insecticide activity to diptera larvae such as
XX aedes. (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 4065 BP; 1471 A; 595 C; 752 G; 1247 T; 0 U; 0 Other;
XX
```

Query Match 13.2%; Score 789; DB 1; Length 4065;
Best Local Similarity 68.0%; Pred. No. 5.3e-134;
Matches 1171; Conservative 0; Mismatches 520; Indels 30; Gaps 4;

```
QY 2292 AATAAGCGAAAAGGTTGTGAGTCCCTATGTTTACAAAGTAGTAGCAAAAAATACGTTAAAAA 2351
DB |||||
QY 2277 AATCAGAACGAGAAGTTGTGAATGCATGTTTACAAATGACGCGAAGATGCATTAACA 2336
DB |||||
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGATGTCAGATG 2411
DB |||||
QY 2337 TTGGAACGACAGATTATGACATAGATCAAGCGCCAAATCTTTGGAATGATTTCTGAAG 2396
DB |||||
QY 2412 AACAAAATCCTCAGGAAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471
DB |||||
QY 2397 AATTATATCAAAAGAAAATAATGCTGTTATAGATGAAATTAATAATGCGAAACAACTTA 2456
DB |||||
QY 2472 GTCAGTCTCGTAACTTACTCTCAAAATGGAGACTTT-----TCTGGGAATGATGGACAT 2525
DB |||||
QY 2457 GTCAATCTCGAATGTACTTCAAAACGGGATTTTGAATCGGCTACGCTTGGTTGACAA 2516
DB |||||
QY 2526 TCGGTAATGATATATCATAGGATCCAAATTAATCTTATTTTAAAGAAAATTTCTACAGA 2585
DB |||||
QY 2517 CAAGTGATAATATCAAAATTCAAAGAGATGATCCTATTTTAAAGGGCATTTACCTTCATA 2576
DB |||||
QY 2586 TCGGTGACGACGAGACATATATGGAACCTTATTTCCACCTATATCTCTCAAAAATAG 2645
DB |||||
QY 2577 TGTCTGGGCGGAGAGACATTTGATGGTACGATATTTCCGACCTATATATTTCCAAAATTTG 2636
DB |||||
QY 2646 ATGAGTCTAAATTTAAACCATATACACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTA 2705
DB |||||
QY 2637 ATGAATCAAAATTTAAACCGTATACAGTTTACCTAGTAGGGGATTTGTAGGAAGTAGTA 2696
DB |||||
QY 2706 AAGATTTGAAATTTAATGGTAAACAGTTACGGGAAAGAAATGATGCTATCATGAATGTTTC 2765
DB |||||
QY 2697 AAGATGTAGAACTAGTGGTTTCAACGCTATGGGGAAGAAATGATGCGCATCATGAATGTTTC 2756
DB |||||
QY 2766 CAAATGATTTGGCCTATATGACGCTTAATCCCTCATGTCGAGATTTATCGCTGTGAATCAT 2825
DB |||||
QY 2757 CAGCTGATTTAAACTATCTGTATCTCTTCTACCTTTGAT-----TGTGAAGGGT 2804
DB |||||
QY 2826 CGTCTCAGTATGTGAGCCAAAGGTTATCTTACACCAACAGATGGATATGCTCCCGATATGT 2885
DB |||||
QY 2805 CTAATCGTTGTGAGCGTCCGCTGTCGCGCTTAACTTGGGAACACTTCTGATATGTTGT 2864
DB |||||
QY 2886 ATGCATGCCCGGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGATCGTCAATTTTC 2945
DB |||||
QY 2865 ATTCATGCCAATATGATACAGGGAAGAAAGCATGTGATGTGCTGAGGATTTCCCATCAATTTA 2924
DB |||||
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Db 2148 GGATTTTGAATCGGCTACGCTTGGTGGACAAACAAGTGATAATATCAAAATTCAGGAAGA 2207
Qy 2554 TAATCCTATTTTAAAGGAAATTTCTACAGATCGGTGGACGACGACATATATGGAAC 2613
Db 2208 TGATCCTATTTTAAAGGCAATTAACCTTCATATGCTCGGGGCGAGACATTTGATGGTAC 2267
Qy 2614 TCTATTTCCAACTTATCTGTCAAAATATAGATGAGTCTAAATTTAAATCCATATACACG 2673
Db 2268 GATATTTCCGACCTATATTTCCAAATTTGATGAATCAAAATTTAAACCGTATACACG 2327
Qy 2674 TTATCGAGTAGAGGGTTTGGGAAGTAGTAAGATTTGAAATTAATAGTTAAACAGCTTA 2733
Db 2328 TTACTAGTAAGGGGATTTGTAGGAAGTAGTAAGATTTGAAATTAATAGTTAAACAGCTTA 2387
Qy 2734 CGGGAAGAAATTCATGCTATCATGAATTTTCCAAATGATTTGGCTATATCGAGCCCTAA 2793
Db 2388 TGGGAAGAAATTCATGCTATCATGAATTTTCCAGCTGATTTAAACATATCTGTATCTTC 2447
Qy 2794 TCCTTCATGTGGAGATTCATGCTGTGAATCATGCTCTCAGTATGTGAGCCAAAGGGTATCC 2853
Db 2448 TAC-----CTTTGATTGTGAAGGCTCTAATCGTTGTGAGACGTCGCGTGTGCC 2495
Qy 2854 TACACCAACAGATGATATGCTCCGATATGTATGATGCGCGCAAAATATAGATAGAAA 2913
Db 2496 GGCTAACATTTGGGAACACTTCTGATATGTTGATTTTCATGCAATATGATACAGGGAATA 2555
Qy 2914 GCATGTGAAGTGTCAACGATCGTCACTCATTTGATTTTTCATATTCACACCGGAGAGTAGA 2973
Db 2556 GCATGTCGTATGTCAGGATTCCTCAATCAATTTAGTTTTCATATGATACAGGGGATTAGA 2615
Qy 2974 TACAAATPACAAATGTAGTATGATGCTTTTAAATTAATTTCTAATCCAGATGGATACGC 3033
Db 2616 TACAAATGAAATATAGSGGTTTGGGTCATGTTTAAATATCTTCTCCAGATGGATACGC 2675
Qy 3034 TACAGTAGGAATCTAGAGTCATTTGAAGAGGACCACTAACAGGTGAAGCATTTGGCACA 3093
Db 2676 ATCATTAGATAAATTTAGAGTAATTTGAAGAGGCGCAATAGATGGGGAAGCACTGTCAAC 2735
Qy 3094 TGTGAACAAAGGAAAGAAATGGAACCAACATGAGGAAAGAAAGCTTTGGGAAACACA 3153
Db 2736 CGTGAACACATGGAAGAAATGGAACGATCAATGGAAGCAAAAGCTTGGGAAACACA 2795
Qy 3154 ACAAGCCTATGATCAGCAAAACAGGCTGTAGATGCAATTTTACAAATGAAACAAGA--- 3210
Db 2796 ACAAGCATATGATGAGGAAACAGGCAATGATGCTTTTATTCACAAATGTAACAGATGA 2855
Qy 3211 ---GTTACACTATCATTAATCTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTC 3267
Db 2856 GGCTTTACAGTTTGTATACGACACTCGCTCAAAATTCAGTACGCTGAGTATTTGGTACAATC 2915
Qy 3268 GATTTCCCTATGATACCAATATTTGTTTACCGAATGCTCCAGGTATGAACTATCATGTATA 3327
Db 2916 GATTTCCATATGTTGACAAATGATTTGTTGTCAGATGTTCCAGGTATGAAATTTATGATATCTA 2975
Qy 3328 TCAAGAGTTAAACGACGATTCATGCAAGGTTTAAATTTATATGATGACGAAATGTCTAT 3387
Db 2976 TGTAGAGTTGATGACGAGTGGCACAAGCGCTTATTTGATGATACAGAAATATAT 3035
Qy 3388 AACAAATGGTGACTTTACACAGGATTTACAGGATGGCAGCAACAGAAATGCCGGGT 3447
Db 3036 TAAAAATGGTGATTTTACACAAAGGGGTAATGGGGTGGCATGTAACTGGAATTCAGACGT 3095
Qy 3448 ACAACAAATGGATGGAGCTTCAGTATTTAGTTTCTATCAAAATGAGCGCGGGGTATCTCA 3507
Db 3096 ACAACAAATAGATGGTGTCTGTATTTGTTTCTATCTAATTTGAGGTGCTGGCGGTATCTCA 3155
Qy 3508 AAACTTGCATGCTCAAGATCATCATGATATGTTGTTACGTGTGATTCGCAAAAGAAAGG 3567
Db 3156 AATGTCCATCTCCAACATATCATGGGTATGTTCTTACGTGTTATTTGCCAAAAGAGG 3215
Qy 3568 ACCTGGAAGAGGTATGTAACGATGATGATTTGATTTGAAAGCAGGAAACACTTAAGTT 3627
Db 3216 ACCTGGAATGGGTATGTCACGCTTATGGATTGTGAGGAGAAATCAAGAAATTTGACGTT 3275

Qy 3628 CACTTCTTGGAAAGGATATATGACAAACACAGTAGAGGTATTTCCAGAAAGTATCG 3687
Db 3276 TAGCTCTTGTGAAGAGGATATATACGAAGACAGTAGATGTATTTCCAGATACAGATCG 3335
Qy 3688 TGTACCGATTGAAATAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCT 3747
Db 3336 TGTACGAAATTGAGTAGGCGAAACCGAAGGTTGTTTATATCGAAGCATTTGATTAAT 3395
Qy 3748 TTGTATGCAAGGATATGATTAACAATATAAC 3778
Db 3396 TTGCATGAACGAGTGATTAATAAAAAATACC 3426

RESULT 12
AAN96139
ID AAN96139 standard; DNA; 4184 BP.
XX
AC AAN96139;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 15-MAY-1990 (first entry)
XX
DE Bacillus thuringiensis israelis strain toxin.
XX
KW Bacillus thuringiensis, israelensis strain; toxin; diptera larvae; aedes.
XX
OS Bacillus thuringiensis; israelensis.
XX
FH Key Location/Qualifiers
FT CDS 461..3867
FT /tag= a
FT /product= "toxin"
XX
PN JP01080294-A.
XX
PD 27-MAR-1989.
XX
PF 21-SEP-1987; 87JP-00238394.
XX
PR 21-SEP-1987; 87JP-00238394.
XX
PA (SUMO) SUMITOMO CHEM IND KK.
PA (MARU-) MARUBENI KK.
XX
DR WPI; 1989-134798/18.
DR P-PSDB; AAP93308.
XX
PT Insecticide protein gene - from Bacillus thuringiensis israelensis
PT strain, used to produce protein toxic to diptera larvae, eg. aedes.
XX
PS Fig 2(1) - 2(3); pages 639-40; 8pp; Japanese.
XX
CC The gene is used to produce protein toxic to diptera larvae, e.g. aedes.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 4184 BP; 1501 A; 627 C; 774 G; 1282 T; 0 U; 0 Other;

Query Match 13.1%; Score 781.8; DB 1; Length 4184;
Best Local Similarity 68.2%; Pred. No. 1.1e-132;
Matches 1173; Conservative 0; Mismatches 517; Indels 31; Gaps 5;
Qy 2292 AATAACGGAAGGTTGTGAGTCCATGTTTACAAAGTAGTAGCAAAAAATACGTTAAAAA 2351
Db 2397 AATCAGACGAGAGTTGTGAATGCACTGTTTACAATGACGGAAGATGCATTAAACA 2456
Qy 2352 TAGAAAACGACAGATTATGAAATAGATCAAGCGGCCCATTTCTATAGAAATGTATCTCAGATG 2411
Db 2457 TTGGAACGACAGATTATGACATAGATCAAGCCGCAAAATCTTGTGGAATGTATTCTTGAAG 2516

PT gene library from plasmid deoxyribonucleic acid, etc.

XX Disclosure; Page ?; 9pp; Japanese.

XX A plasmid contg. the gene is isolated by forming a gene library from
CC plasmid DNA of *B. thuringiensis israelensis* (HD 522 strain, USA Goldberg
CC ONR60) followed by screening with anti-*israelensis* insecticidal protein
CC IG. The insecticidal protein is highly effective against *Diptera*, esp.
CC *Aedes*. (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 4934 BP; 1797 A; 749 C; 877 G; 1511 T; 0 U; 0 Other;

Query Match 13.0%; Score 774.6; DB 1; Length 4934;

Best Local Similarity 71.4%; Pred. No. 2.2e-131;

Matches 1071; Conservative 0; Mismatches 404; Indels 24; Gaps 3;

QY 2292 AATAAGCGAAAAAGGTTGTGAGTCTATGTTTACAGTAGTACGAAAAATACGTTAAAAA 2351

DB 3440 AACAGGTACAAACAATAATTAATACATTTTATGCAATCCTATAAAAAACACTTTACAAT 3499

QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCATTTCTATAGATGTATGTCAGATG 2411

DB 3500 CAGAACTTACAGATTATGACATAGATCAGCGGCAATCTTGTGGAATGATTTCTGAAG 3559

QY 2412 AACAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471

DB 3560 AATTATATCAAAAGAAAAAATGCTGTTATTAGATGAAGTTAAATAATGCGAAACAACTTA 3619

QY 2472 GTCAGTCTGTAATCTACTCAAAAATGGAGACTTT-----TCTGGGAATGATGGACAT 2525

DB 3620 GTCAATCTCGAAATGTACTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAA 3679

QY 2526 TCGGTATGATATTATCATAGGATCCAAATATCTATTTTCCAACTTATCTGTCAAAAAATAG 2645

DB 3680 CAAGTGATATATCACAATTCAGAGATGATCTATTTTAAAGGGCATTAACCTTCATA 3739

QY 2586 TCGGTGAGCAGACATATATGGAATCTTATTTCCAACTTATCTGTCAAAAAATAG 2645

DB 3740 TGTCTGGGCGAGACATTTGATGGTACGATATTTCCGACCTATATATTCNAAAATTTG 3799

QY 2646 ATGAGTCTAAATTAACCATATACAGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 2705

DB 3800 ATGAATCAAAATTAACACCGTATACACGTTACCTAGTAAGGGATTTGTAGGAAGTAGTA 3859

QY 2706 AAGATTTGAAATTAATGGTAACAGTTTACGGGAAAGAAATTTGATGTCATCATCAATGTTTC 2765

DB 3860 AAGATGTAGAACTAGTGGTTTACGCTATGGGGAAGAAATTTGATGCCATCATGAATGTTTC 3919

QY 2766 CAAATGATTTGGCTATATGACGCTTAATCCTTTCATGTGGAGATTATCGCTGGAATCAT 2825

DB 3920 CAGCTGATTTAAACTATCTGATCCTTCTAC-----CTTTGATTTGGAAGGTT 3967

QY 2826 CGTCTCGATGTGAGCGCAAGGATTCCTACACCAACAGATGGATATGCTCCCGATATGT 2885

DB 3968 CTAATCGTTGTGAGACGTCGCGCTGTGCGGCTAACATTTGGGAACACTTCTGATATGTTGT 4027

QY 2886 ATGCATGCCGCAAAATATAGATAGAAGCATGTGAAGTGTACAGTGTGTCAGTATGCTCCATTTC 2945

DB 4028 ATTCATGCCAATATGATACAGGGAAGAAAGCATGTGATGTGAGGATTCCTCAATCAATTA 4087

QY 2946 ATTTTCATATTTGACACCGGAGAAGTAGATACAAATACAAATGTAGTATTTGATGTTCTTAT 3005

DB 4088 GTTTCACTATTGATACAGGGGCATTAGATACAAATGAAATATAGGGGTTTGGGTCATGT 4147

QY 3006 TAAAAATTTCTAATCCAGATGGATAGCTACAGTAGGGAAATCTAGAAGTCATTGGAAGAAG 3065

DB 4148 TTAATAATATCTTCTCCAGATGGATAGCGCATCATTAGATAATTTAGAAGTAATTTGAAGAAG 4207

QY 3066 GACCACCTAACAGGTGAAGCAATTCGCACATGTGAAACAAAGGAAGAAAGAAATGGAACAC 3125

DB 4208 GGCATATAGATGGGAAGCACTGTACGGGTGAAACACATGGAGGAAGAAATGGAACGATC 4267

QY 3126 ACATGGAGAAAAACGTTGGGAAACACAAACAGCCTTATGATCCAGCAAAACAGGCTGTAG 3185

DB 4268 AATGGAGCAAAACGTTCCGAAACACACAAACGATATGATGTAGCGAAACAGCCATTG 4327

QY 3186 ATGCAATTTTACAAATGAACAAGA-----GTTACACTATCATATTTACTTTAGATCATTA 3239

DB 4328 ATGCTTTTATTCACAAATGTACAAAGATGAGGCTTTACAGTTTGTATCGACACTCGCTCAAA 4387

QY 3240 TTCAAAACGCTGATCGACTGGTACAGTCCGATTCCTTATGTTATACCATTAATTTGGTTACCGA 3299

DB 4388 TTCAAGTACGCTGAGTATTTGGTACAATCGAATTCATATGTGTACAATGATTTGGTTGTCAG 4447

QY 3300 ATGCTCCAGGTATGAACATGATGATATCAAGAGTTTAAACGCAACGCTTATCATTCGAAGGTT 3359

DB 4448 ATGTTCCAGGTATGAATTTATGATATCTATGTAGTGGTGGATGACGAGTGGCAACAGCGC 4507

QY 3360 ATAAATTTATGATGACGAAATGTCAATAACAAATGGTGTGATTTTACAAAGGATTTACAGG 3419

DB 4508 GTTATTTGTATGATCAAGAAATATTTATTTAAAAATGGTGTATTTTACAAAGGGGTATATGG 4567

QY 3420 GATGGCACCAACAGGAAATGCCCGGTACACAAATGGATGGAGCTTCAGTATTAGTTTC 3479

DB 4568 GGTGGCATGTAACTCGGAAATGACAGCGTACACAAATAGATGGTGTCTGTATTGGTTTC 4627

QY 3480 TATCAAAATGGAGCGCGGGGGTATCTCAAAACCTTGATGCTCAAGATCATCATGGATATG 3539

DB 4628 TATCTAATTTGGAGTGTGCGGTATCTCAAAATGTCCATCTCCAAACATTAATCATGGGTATG 4687

QY 3540 TGTTCAGTGTGATGTCACAAAAGAGAGACCTGGAAAAAGGTTATGTAACGATCATGGATT 3599

DB 4688 TCTTACGTTGTTATGTCACAAAAGAGAGACCTGGAAATGGGTATGTGTCAGCTTATGGATT 4747

QY 3600 GTAATGGAAGCAGGAAACACTTAAGTTCACCTTCTTCCGAGAGGATATATGACAAAAA 3659

DB 4748 GTGAGGAGAAATCAAGAAAAATTTGACGTTTACGCTTTGTGAAGAGGATATATTTACGAAGA 4807

QY 3660 CAGTAGAGGTATTTCCAGAAAAGTGTGTCGGAATTTGAAATAGGAGAAACCGAAGGTA 3719

DB 4808 CAGTAGATGTTTCCAGATACAGATCGTGTACGAATTTGATAGAGGAAACCGAAGGTT 4867

QY 3720 CATTTTATATAGATACATCGAGTTGCTTTGTATGCAAGGATATGATAAATAAATAAC 3778

DB 4868 CGTTTTATATCGAAAGCATTTGAATTAATTTGATGAAACGAGTGAATTAATAAATAAATAAC 4936

RESULT 14

AAQ81178
ID AAQ81178 standard; DNA; 3543 BP.

XX AAQ81178;

XX AC
XX 25-MAR-2003 (revised)

DT 12-AUG-1995 (first entry)

XX B.t. toxin PS71M3 gene.

XX Delta-endotoxin; crystal protein; biological control agent; Calliphorid;
KW screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide;
KW pesticide; B.t.; ss.

XX *Bacillus thuringiensis*.

XX WO9502694-A2.

XX 26-JAN-1995.

XX 13-JUL-1994; 94WO-US007902.

XX 15-JUL-1993; 93US-00093199.

XX (MYCO) MYCOGEN CORP.

XX Hickie LA, Payne J;

XX

	Qy	3066	GACCACTAACAGGTGAAGCATTGGCCATCATGTTGAAACAAGAAGAAAAGAAATGAAACAAC	3125
	Dd	2840	GGCCAATAGATGGGGAAGCACCTGTCCCGCTGAAAACACATGGGAAGAATAATGGAACGCATC	2899
	Qy	3126	ACATGGAGAAAAAACCCTTGGGAAACAACAACAGCCCTATGATCCAGCAAAAACAGCTCTGTAG	3185
	Dd	2900	AATGGNAGCNAAACGTTTCGAAAACACACACAGCATATGATGTAGCGNAACAAGCCATTYA	2959
	Qy	3186	ATGCATTATTTTACAAATGAACAAGA-----GTTACACTATCATATATPACTTTTAGATCATTA	3239
	Dd	2960	ATGCTTTATTTTCACAAATGTACAAGATGAGGCCCTTTACAGTTTGTATACGACACTCGCTCAAA	3019
	Qy	3240	TTCAAAACCGCTGATCGACTGGTACAGTCCGATTCCTTATGTATACCATTAATTTGGTTACCGA	3299
	Dd	3020	TTCAGTACGCTGAGTATTTGGTACAATCGAATCCATATGTGTACAATGATTTGGTTGTTCAG	3079
	Qy	3300	ATGCTCCAGGTATGAACATATGATGTATATCAAGAGATTAAACGCAAGCTATCATGCAAGGTT	3359
	Dd	3080	ATGTTCCAGGTATGAATTTATGATATCTATGTAGAGTTGGATGCAAGTGCCACAAGCGC	3139
	Qy	3360	ATAATTATATGATGACGAAATGTCTATAACAATGGTGACTTTTACACAAGGATTACAGG	3419
	Dd	3140	GTTATTTGTATGATACAAGAAATATTATTAAAAAATGGTGAATTTTACACAAGGGGTAAATGG	3199
	Qy	3420	GATGGCAGCAACAGGAAATGCCCGGTACAACAATGGATGGAGCTTCAGTATTAGTTTC	3479
	Dd	3200	GGTGGCATGTAACTGGANAATGCAGACGTACACACAATAGATGGTGTCTGTATTGGTTTC	3259
	Qy	3480	TATCAAATTGGAGCGCGGGGTTATCTCAAACCTTGATGCTCAAGATCATCATGGATATG	3539
	Dd	3260	TATCTAATTGGAGTGTGGCGTATCTCAAAATGTCCATCTCCAACATAATCATGGGTATG	3319
	Qy	3540	TGTTACGTGTGATTGCCAAAAGAGAGGACCTCGAAAAGGGTATGTAAACGATGATGGATT	3599
	Dd	3320	TCATTACGTGTATTGCCAAAAGAGAGGACCTGGAAATGGGTATGTACACCTTATGGATT	3379
	Qy	3600	GTAATGAAAGCAGGAAACAACCTTAAGTTCACTCTTTTCGGAAGAAGGATATATGACAAAAA	3659
	Dd	3380	GTGAGGAGAAATCAAGAAAAAATTCAGCTTTTACGCTTGTGGAAGAAGGATATATTACGAAGA	3439
	Qy	3660	CAGTAGAGGTATTTCCCAGAAAGTGATCGTGATCGGATTGAAATAGGAGAAACCGAAGTTA	3719
	Dd	3440	CAGTAGATGTATTTCCCAGATACAGATCGTGATCGAATTTGAGATAGCGCAAAACCGAAGTTT	3499
	Qy	3720	CATTTTATATAGATAGCATCGAGTTGCTTTTGTATGCAAG	3758
	Dd	3500	CGTTTTATATCGAAGCAATTGAATTAATTTCATGAACG	3538
		RESULT 15		
		AAQ14669	ID	AAQ14669 standard; DNA; 3543 BP.
		XX	AC	AAQ14669;
		XX	AC	AAQ14669;
		DT	27-AUG-2003	(revised)
		DT	25-MAR-2003	(revised)
		DT	04-FEB-1992	(first entry)
		XX	XX	
		DE		Dipteran active toxin gene.
		KW		Insecticide; B.t; crystal; delta endotoxin; cryIVA; ss.
		XX	OS	Bacillus thuringiensis serovar morrisoni.
		XX	XX	
		FH		Location/Qualifiers
		FT		1..3543
		ET		/+tag= a
		XX		
		FN		EP457498-A.
		XX		
		PD		21-NOV-1991.
		XX		

PF 09-MAY-1991; 91EP-00304180.
 XX 15-MAY-1990; 90US-00524255.
 PR 01-OCT-1990; 90US-00590903.
 XX (MYCO) MYCOGEN CORP.
 PA Sick AJ;
 XX WPI; 1991-341902/47.
 DR P-PSDB; AAR14373.
 XX
 XX Bacillus thuringiensis genes encoding diptera-active toxins - and
 PT transformed microbes used to control insects in various environments.
 PS Claim 1; Page 10; 20pp; English.
 XX
 CC The sequence was obtd. from plasmid pMYC1625 which was isolated from a
 CC genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69
 CC (NRRL B-18515)]. It is related to the cryIVA family of genes, the 140 kD
 CC endotoxin gene and the type II gene from B.t. var. israelensis. The gene
 CC encodes a 130 kD protein. Microorganisms transformed with the DNA may be
 CC administered to dipteran insects or their environments, the expressed
 CC toxins acting as an insecticide. See also AAQ14670-Q14672. (Updated on 25
 CC -MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 3543 BP; 1278 A; 567 C; 612 G; 1086 T; 0 U; 0 Other;

Query Match 12.8%; Score 764.2; DB 2; Length 3543;
 Best Local Similarity 71.5%; Pred. No. 1.7e-129;
 Matches 1057; Conservative 0; Mismatches 398; Indels 24; Gaps 3;

QY 2292 AATAAGCGAAAAGTTGTGAGTCCTATGTTTACAGTAGTACGAAAATACGTTAAAAA 2351
 DB |||||
 QY 2072 AAACAGTACAAACAAATAAATAACATTTTATGCAATCTTATAAAACACATTACAAT 2131
 DB |||||
 QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCATTCTTATAGAAATGATGTGACAGTG 2411
 DB |||||
 QY 2132 CAGAACTTACAGATTATGACATAGATCAAGCCGCAATCTTGTGGAATGATTTCTTGAAG 2191
 DB |||||
 QY 2412 AACAAATCTCAGGAAAAAATAATGTTATGGATGAATAAATGCGCAAAACAACTTA 2471
 DB |||||
 QY 2192 AATTATATCAAAAGAAAAAATGCTGTTATTAGATGAAGTTAAAAATGCGAAACAACTTA 2251
 DB |||||
 QY 2472 GTGAGTCTGTAATCTACTCCAAATGGAGACTTT-----TCTGGGAATGATGGACAT 2525
 DB |||||
 QY 2252 GTCAATCTCGAAATGTACTTCAAAACGGGGAATTTGAATCGGCTACGCTTTGGTGACAA 2311
 DB |||||
 QY 2526 TCGGTAATGATATTATCATAGGATCCAATAATCCTATTTTAAAGGAAAAATTTCTACAGA 2585
 DB |||||
 QY 2312 CAAGTGATATATCACAATTCAGAGAGATGATCCTATTTTAAAGGGCATTACCTTCATA 2371
 DB |||||
 QY 2586 TGGGTGAGCAGCAGACATATATGGAACCTTATTTCCAACTATATCTGTCAAAAAATAG 2645
 DB |||||
 QY 2372 TGTCTGGGGCGAGAAAATGATGGTAGCATATTTCCGACCTATATATTTCCAAAAAATG 2431
 DB |||||
 QY 2646 ATGAGTCTAAATTAACCAATATACAGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTA 2705
 DB |||||
 QY 2432 ATGAATCAAAATTAACCAATATACAGTTATCGAGTAAGAGGGATTTGTAGGAAGTAGTA 2491
 DB |||||
 QY 2706 AAGATTGAAATTAATGGTAACAGTTTACGGGAAAGAAATTTGATGCTATCATCAATGTTTC 2765
 DB |||||
 QY 2492 AAGATGTAGAACTAGTGGTTTACGGTATGCGGGAAGAAATTTGATGCCATCAATGTTTC 2551
 DB |||||
 QY 2766 CAAATGATTTGGCCTATATACAGCCCTAAATCCTTTATGTTGGAGATTAATCGCTGTGAATCAT 2825
 DB |||||
 QY 2552 CAGCTGATTTAAACTATCTGTATCTCTTAC-----CTTTGATTGTGAAGGTT 2599
 DB |||||
 QY 2826 CGTCTCAGTATGTGAGCCAGGGTATCTTACCAACAGATGGATGATGCTCCCGATATGT 2885
 DB |||||
 QY 2600 CTAATCGTTGTGAGCGTCCGCTGTGCGCGGTAAACATTTGGGAACACTTCTGTATGTCGT 2659
 DB |||||

QY 2886 ATGATGCGCGCAAAATATAGATAGAAAGCATGTGAAGTGTACAGTCTGTCATCCATTTG 2945
 DB |||||
 QY 2660 ATTTCATGCCAATATGATACAGGAAAAGCATGTGATGTTCAGGATTCCTCAATTTA 2719
 DB |||||
 QY 2946 ATTTCATATTGACACCGGAGAGTAGATACAAATACAAATGATGATGATGATGATGAT 3005
 DB |||||
 QY 2720 GTTTCATATTGATACAGGGGCATTAGATACAAATGAAATATAGGGTTTGGGTCTGT 2779
 DB |||||
 QY 3006 TAAATATTTCTAATCCAGATGGATGATGATGATGATGATGATGATGATGATGATGAT 3065
 DB |||||
 QY 2780 TTAATATATCTCTCCAGATGGATGATGATGATGATGATGATGATGATGATGATGAT 2839
 DB |||||
 QY 3066 GACCACTAACAGGTGAAGCATTTGGCACTGTGAAACAAAGAAAGAAAGAAAGAAAGAA 3125
 DB |||||
 QY 2840 GGCAATAGATGGGGAAGCACTGTCAAGCGTGAAACACATGGAGAGAAATGAAACGATC 2899
 DB |||||
 QY 3126 ACATGAGAGAAAAACGTTGGGAAACACAAAGCCCTATGATCCAGCAAAACAGCGCTGTAG 3185
 DB |||||
 QY 2900 AATGGAAGCAAAACGTTGGGAAACACAAAGCATATGATGTAGCGAAACAAAGCCATTA 2959
 DB |||||
 QY 3186 ATGCATTTTACAAATGAAACAGAA-----GTTACACTATCATATTTTATGATCATTA 3239
 DB |||||
 QY 2960 ATGCTTTATTCACAAATGTACAAAGATGAGGCTTTTACAGTTTGTATACGACACTCGCTCAA 3019
 DB |||||
 QY 3240 TTCAAAACGCTGATCGACTGGTACAGTCCCTATGATACCATTAATTTGTTTACCGA 3299
 DB |||||
 QY 3020 TTCAGTACGCTGATGATTTGGTACAAATCGATTCATATGTTACAAATGATTTGTTGTGAC 3079
 DB |||||
 QY 3300 ATGCTCCAGGTATGAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3359
 DB |||||
 QY 3080 ATGCTCCAGGTATGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3139
 DB |||||
 QY 3360 ATAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3419
 DB |||||
 QY 3140 GTTATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3199
 DB |||||
 QY 3420 GATGGCAGCAACAGGAAATGCGCGGTACAAACAAATGATGATGATGATGATGATGATGATGAT 3479
 DB |||||
 QY 3200 GGTGGCATGTAACGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 3259
 DB |||||
 QY 3480 TATCAAAATGGAGCGCGGGGTATCTCAAAATGTCATCTCAAGATCATCATGATGATGATGAT 3539
 DB |||||
 QY 3260 TATCTAATTTGGAGTGTGCGGTATCTCAAAATGTCATCTCAAAATGTCATCTCAAAATGTCAT 3319
 DB |||||
 QY 3540 TGTTCAGTGTGATTTGCCAAAAGAGGACCTGGAAAAGGGTATGTAACGATGATGATGATGATGAT 3599
 DB |||||
 QY 3320 TCTTACGTGTATTGTCNAAAAGAGGACCTGGAAAATGGGTATGTCACGCTTATGATGATGAT 3379
 DB |||||
 QY 3600 GTAAATGGAAGCAGGAAACACATTAAGTTCACCTTTTGGCAAGAGGATATATGACAAAAA 3659
 DB |||||
 QY 3380 GTGAGAGAAATCAAGAAAATTTGACGTTTACGTTTGTGTAAGAGGATATATTTACGAGA 3439
 DB |||||
 QY 3660 CAGTAGAGGATTTCCAGAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3719
 DB |||||
 QY 3440 CAGTAGATGATTTCCAGATACAGATCGTGTACGAATTCAGATAGGCGAAACCGAAGGTT 3499
 DB |||||
 QY 3720 CATTTTATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3758
 DB |||||
 QY 3500 CGTTTTTATATCGAAAAGCATTTGAATTAATTTTGTGATGATGATGATGATGATGATGATGAT 3538
 DB |||||

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Job time : 2221.9 secs

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:48:03 ; Search time 2957.36 Seconds
(without alignments)
16721.276 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5980	100.0	5980	8	US-10-781-979-1
2	2082	34.8	2082	8	US-10-781-979-2
3	2073	34.7	2073	8	US-10-781-979-4
4	1686	28.2	1686	8	US-10-781-979-6
5	967	16.2	4391	9	US-10-929-754-4
6	855	14.3	2145	8	US-10-782-141-1
7	789	13.2	3684	9	US-10-929-754-2
8	747	12.5	2019	8	US-10-782-141-2
9	739.8	12.4	2010	8	US-10-782-141-4
10	390	6.5	4359	5	US-10-120-544A-3
11	390	6.5	4359	10	US-11-091-654-3
12	380.8	6.4	3504	5	US-10-089-678-2
13	380.8	6.4	3504	5	US-10-089-678-3
14	318.6	5.3	4366	5	US-10-120-544A-19
15	318.6	5.3	4366	10	US-11-091-654-19
16	313	5.2	4896	6	US-09-756-526A-3
17	313	5.2	4896	6	US-10-345-020-3
18	313	5.2	4896	6	US-10-342-821-3
19	312.2	5.2	4359	5	US-10-120-544A-17
20	312.2	5.2	4359	10	US-11-091-654-17
21	310.4	5.2	6930	3	US-09-756-526A-1
22	310.4	5.2	6930	6	US-10-345-020-1
23	310.4	5.2	6930	6	US-10-342-821-1

24	308.2	5.2	4188	5	US-10-120-544A-5	Sequence 5, Appli
25	308.2	5.2	4188	10	US-11-091-654-5	Sequence 5, Appli
26	307	5.1	3621	5	US-10-032-717-1	Sequence 1, Appli
27	307	5.1	3621	6	US-10-414-637-1	Sequence 1, Appli
28	307	5.1	3621	7	US-10-606-320-1	Sequence 1, Appli
29	307	5.1	3621	8	US-10-746-914-1	Sequence 1, Appli
30	307	5.1	3621	10	US-11-021-115-5	Sequence 5, Appli
31	307	5.1	3633	5	US-10-032-717-3	Sequence 3, Appli
32	307	5.1	3633	6	US-10-414-637-3	Sequence 3, Appli
33	307	5.1	3633	7	US-10-606-320-3	Sequence 3, Appli
34	307	5.1	3633	8	US-10-746-914-3	Sequence 3, Appli
35	307	5.1	4874	5	US-10-032-717-27	Sequence 27, Appli
36	307	5.1	4874	6	US-10-414-637-27	Sequence 27, Appli
37	307	5.1	4874	7	US-10-606-320-17	Sequence 17, Appli
38	307	5.1	4874	8	US-10-746-914-17	Sequence 17, Appli
39	307	5.1	6613	5	US-10-032-717-28	Sequence 28, Appli
40	307	5.1	6613	6	US-10-414-637-28	Sequence 28, Appli
41	307	5.1	6613	7	US-10-606-320-18	Sequence 18, Appli
42	307	5.1	6613	8	US-10-746-914-18	Sequence 18, Appli
43	279.2	4.7	3507	7	US-10-614-524-3	Sequence 3, Appli
44	278	4.6	3465	10	US-11-018-615-26	Sequence 26, Appli
45	275.6	4.6	3471	5	US-10-099-285-71	Sequence 71, Appli

ALIGNMENTS

RESULT 1
US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozielec, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-781-979-1

Query Match	100.0%;	Score 5980;	DB 8;	Length 5980;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5980;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TACATGCAATACATAAAGAGAGGTTTAAAAATCAATCACTACCTACCCACAAAATAATCGGTT	60	
Db	1	TACATGCAATACATAAAGAGAGGTTTAAAAATCAATCACTACCTACCCACAAAATAATCGGTT	60	
QY	61	TATTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATATATAGAAAGACAC	120	
Db	61	TATTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATATATAGAAAGACAC	120	
QY	121	CTAACATATATTTATTAGTGCTTTAAAAATAGGACTATATAAGGAGTGAAAAAGATGA	180	
Db	121	CTAACATATATTTATTAGTGCTTTAAAAATAGGACTATATAAGGAGTGAAAAAGATGA	180	
QY	181	GTCCATATCAAAATAAAATGAATATGAATTTGGAATCCTCATCGAATACACAATA	240	
Db	181	GTCCATATCAAAATAAAATGAATATGAATTTGGAATCCTCATCGAATACACAATA	240	
QY	241	CGCCAAACAGATATCTCTTTTGC AAAATAATCGGGATATGTCTACTATGTCTTGAATGATT	300	

|||||
241 CGCACAACAGATATCCTTTGCAAAATAATCGGATATGCTACTATGTCTGGAAATGATT 300
QY
301 GTCAGGGAATCTCATCGGATGAATTTGGGAATCAGTCGAAACGATAACAAAGTATTGGGA 360
Db
301 GTCAGGGAATCTCATCGGATGAATTTGGGAATCAGTCGAAACGATACAAAGTATTGGGA 360
QY
361 TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTATCAA 420
Db
361 TAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTATCAA 420
QY
421 TAATAGGAATACTAATTCGACTAATCGTCAAACTGTGTCAGCACCTTCTATATGTGATT 480
Db
421 TAATAGGAATACTAATTCGACTAATCGTCAAACTGTGTCAGCACCTTCTATATGTGATT 480
QY
481 TATTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCGAGATT 540
Db
481 TATTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGATGCGATTGCGAGATT 540
QY
541 TTGACCGTAAATTTGAAAAATTTATAGAGATTAATCTTTCTTATCTTGGGGCTTGGCTTA 600
Db
541 TTGACCGTAAATTTGAAAAATTTATAGAGATTAATCTTTCTTATCTTGGGGCTTGGCTTA 600
QY
601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGGACAAATTAGTTTATTATT 660
Db
601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGGACAAATTAGTTTATTATT 660
QY
661 TTAACCTTTTCAGAAAGAGATTTTCAATGAAATTCCTAGGAGGTCAATTTGTCAAGAAACAATG 720
Db
661 TTAACCTTTTCAGAAAGAGATTTTCAATGAAATTCCTAGGAGGTCAATTTGTCAAGAAACAATG 720
QY
721 CTCAGATATGTTTATTAACCTTTCACAAAGTCAAGTCAAAATGTCAGTTTATTAATAATA 780
Db
721 CTCAGATATGTTTATTAACCTTTCACAAAGTCAAGTCAAAATGTCAGTTTATTAATAATA 780
QY
781 GGGATCGAGTTCAATATAAGACCAATGTTCCCATTTTACCGGTGATTAATGAGTGCAGGAATGTAAGT 840
Db
781 GGGATCGAGTTCAATATAAGACCAATGTTCCCATTTTACCGGTGATTAATGAGTGCAGGAATGTAAGT 840
QY
841 CGGAAATTAATATACCTTAACAGTGGTTGTGATTTTACCGGTGATTAATGAGTGCAGGAATTA 900
Db
841 CGGAAATTAATATACCTTAACAGTGGTTGTGATTTTACCGGTGATTAATGAGTGCAGGAATTA 900
QY
901 AATGCAAAACGGCAGAGTATACCAATTAATGTTTATTAATGTTATCAGGTAGGTTTAAATC 960
Db
901 AATGCAAAACGGCAGAGTATACCAATTAATGTTTATTAATGTTATCAGGTAGGTTTAAATC 960
QY
961 AGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAATTTAATTAATTTTCGTAGAG 1020
Db
961 AGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAATTTAATTAATTTTCGTAGAG 1020
QY
1021 AAATGACGTTGGCGGTATTGGATATTATCGCTATATTCCAACTTATGATTTTGGAAAT 1080
Db
1021 AAATGACGTTGGCGGTATTGGATATTATCGCTATATTCCAACTTATGATTTTGGAAAT 1080
QY
1081 ATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTATACAGATGCAAGTGGGATATT 1140
Db
1081 ATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTATACAGATGCAAGTGGGATATT 1140
QY
1141 CATCGGGAACCTTATAGTTGTTACGGNAATTTGGCCCTAATCTTTTAAATTTGAGGCTTA 1200
Db
1141 CATCGGGAACCTTATAGTTGTTACGGNAATTTGGCCCTAATCTTTTAAATTTGAGGCTTA 1200
QY
1201 ATGGAACACGGGACCTGGTTTATAGTTTACCTTGGCTTAGCAAAATAGGTATATATAATGAGT 1260
Db
1201 ATGGAACACGGGACCTGGTTTATAGTTTACCTTGGCTTAGCAAAATAGGTATATATAATGAGT 1260
QY
1261 ATGTTTCGAGATATTTTGGCGGTGGGTAGGAATCTCGTCAATTAAGAGACTACAAAGG 1320
Db
1261 ATGTTTCGAGATATTTTGGCGGTGGGTAGGAATCTCGTCAATTAAGAGACTACAAAGG 1320
QY
1321 GTAAACGGTATTTTCAACGATGCTCTGGAACTACGAGTAATGATCTACGTAATATTGATT 1380

Db
1321 GTAAACGGTATTTTCAACGATGCTCTGGAACTACGAGTAATGATCTACGTAATATTGATT 1380
QY
1381 TTTAGAAATGCGGATGATATATAAAATTAATCTTCAATTAGCTATCATTAACCTTAGTAGGAGA 1440
Db
1381 TTTAGAAATGCGGATGATATATAAAATTAATCTTCAATTAGCTATCATTAACCTTAGTAGGAGA 1440
QY
1441 CTACCGCTAGACACAGAGTATCGTGTTCAAAGGAGATTTTCGTAGGTAGGGGACCTG 1500
Db
1441 CTACCGCTAGACACAGAGTATCGTGTTCAAAGGAGATTTTCGTAGGTAGGGGACCTG 1500
QY
1501 ATTTAAATTTATGATCGAGTAATTAATGGCTAAGCAGGATGACAATTAATGATCTAGCTTCC 1560
Db
1501 ATTTAAATTTATGATCGAGTAATTAATGGCTAAGCAGGATGACAATTAATGATCTAGCTTCC 1560
QY
1561 CACTTTGATTTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCGGAT 1620
Db
1561 CACTTTGATTTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCGGAT 1620
QY
1621 GTTGTGTATATGGAACCTCCAGAGTTAAAGTATATGTTTGGAGACATACAAGTTTAAAC 1680
Db
1621 GTTGTGTATATGGAACCTCCAGAGTTAAAGTATATGTTTGGAGACATACAAGTTTAAAC 1680
QY
1681 GTGAAATATATTTCAAGCCAATCAAAATTTACAAATACCGGCGGTGAAGTTTATACC 1740
Db
1681 GTGAAATATATTTCAAGCCAATCAAAATTTACAAATACCGGCGGTGAAGTTTATACC 1740
QY
1741 TTTCAAAATTTATCTTCTAATGCTATACCTATGTAATTAAGGCACTCATACAGTGGGG 1800
Db
1741 TTTCAAAATTTATCTTCTAATGCTATACCTATGTAATTAAGGCACTCATACAGTGGGG 1800
QY
1801 ATTTAAATCGGTTTTTAAAGCAAAATCAGAGTATAACGAGTTTATGCAAGTGGCGAA 1860
Db
1801 ATTTAAATCGGTTTTTAAAGCAAAATCAGAGTATAACGAGTTTATGCAAGTGGCGAA 1860
QY
1861 TTAGATTTGATTTAATTAACAAAACCTGAGGACAAAGTTTACCGTATTCGTTTTCTGTTATG 1920
Db
1861 TTAGATTTGATTTAATTAACAAAACCTGAGGACAAAGTTTACCGTATTCGTTTTCTGTTATG 1920
QY
1921 CTGCAAGTAAAGCTCTTTCTTGTAGTATATCTTTTATCCAGGAGTTTGGGGTTCAAAATC 1980
Db
1921 CTGCAAGTAAAGCTCTTTCTTGTAGTATATCTTTTATCCAGGAGTTTGGGGTTCAAAATC 1980
QY
1981 GTTTTGTATCGGTTGAAAAATCTTACTCTGGAATTTATGACGATTTAAATATAGTGATT 2040
Db
1981 GTTTTGTATCGGTTGAAAAATCTTACTCTGGAATTTATGACGATTTAAATATAGTGATT 2040
QY
2041 TTAATTTCTGCTGAAATTTACACCTCCATTAACCTTCAAACTTCAAGTGGATGTGG 2100
Db
2041 TTAATTTCTGCTGAAATTTATCACCTCCATTAACCTTCAAACTTCAAGTGGATGTGG 2100
QY
2101 AGATGCAAGCGAATAGTTTCAATCAGATGTAACCTGTTCTCGACAAAATTTGAATTC 2160
Db
2101 AGATGCAAGCGAATAGTTTCAATCAGATGTAACCTGTTCTCGACAAAATTTGAATTC 2160
QY
2161 TCCCAAGTAAATCAACAACTTTAGAAATAGAGGAGACCGGACCTAGAAAAACAAAGA 2220
Db
2161 TCCCAAGTAAATCAACAACTTTAGAAATAGAGGAGACCGGACCTAGAAAAACAAAGA 2220
QY
2221 ACAGCGTGAACGATCTGTTTACCAATTAATAAATAATTTACTAGAAATAGGTGATT 2280
Db
2221 ACAGCGTGAACGATCTGTTTACCAATTTAAACAAATAATTTACTAGAAATAGGTGATT 2280
QY
2281 GCTGTTTAAACAAATAAGCGAAAAAGGTTGTGAGTCTATGTTTCAAGTAGTACGAAAA 2340
Db
2281 GCTGTTTAAACAAATAAGCGAAAAAGGTTGTGAGTCTATGTTTCAAGTAGTACGAAAA 2340
QY
2341 TACGTTTAAATAGAAAACGACAGATTAATAAGTATCAAGCGGCAATTTCTATAGAAAG 2400
Db
2341 TACGTTTAAATAGAAAACGACAGATTAATAAGTATCAAGCGGCAATTTCTATAGAAAG 2400
QY
2401 TATGTCAGATGAACAAAATCCCTCAGAAAAATAATGTTTATGGGATGAATAAACTGCG 2460
Db
2401 TATGTCAGATGAACAAAATCCCTCAGAAAAATAATGTTTATGGGATGAATAAACTGCG 2460

QY 2461 AAAACAACTTAGTCAGTCTCGTAACTCTACTCCAAATGGAGACTTTTCTCGGAATGATTG 2520
DB |||||
DB 2461 AAAACAACTTAGTCAGTCTCGTAACTCTACTCCAAATGGAGACTTTTCTCGGAATGATTG 2520
QY 2521 GACATTCGGTAATGATATATATATAGATCCAAATTAATCTTATTTTAAAGGAATAATTTCT 2580
DB |||||
DB 2521 GACATTCGGTAATGATATATATAGATCCAAATTAATCTTATTTTAAAGGAATAATTTCT 2580
QY 2581 ACAGATCGGTGGAGCAGACATATATGAACTCTATTTTCCAACTTATCTGTCAAAA 2640
DB |||||
DB 2581 ACAGATCGGTGGAGCAGACATATATGAACTCTATTTTCCAACTTATCTGTCAAAA 2640
QY 2641 AATAGATGAGTCTAAATTTAAATTAATATACACGTTATCGAGTAAAGGGTTTGTGGGAAG 2700
DB |||||
DB 2641 AATAGATGAGTCTAAATTTAAATTAATATACACGTTATCGAGTAAAGGGTTTGTGGGAAG 2700
QY 2701 TAGTAAAGATTTGAAATTAATATGTTAAACGTTACGGGAAAGAAATTAATGATCTATCATGAA 2760
DB |||||
DB 2701 TAGTAAAGATTTGAAATTAATATGTTAAACGTTACGGGAAAGAAATTAATGATCTATCATGAA 2760
QY 2761 TGTTCGAAATGATTTGGCCCTATATGAGCCCTAATCTTCAATGAGGATTTATCGCTGTGA 2820
DB |||||
DB 2761 TGTTCGAAATGATTTGGCCCTATATGAGCCCTAATCTTCAATGAGGATTTATCGCTGTGA 2820
QY 2821 ATCATCTGCTCAGTATGTAGCCAAAGGATATCTTACACCAACAGATGGATATCTCCCGA 2880
DB |||||
DB 2821 ATCATCTGCTCAGTATGTAGCCAAAGGATATCTTACACCAACAGATGGATATCTCCCGA 2880
QY 2881 TATGTATGTCATGCCCGCAAAATATAGATGAAAGCATGTGAAGTGTCAAGTGTCAAGTGTCAATCC 2940
DB |||||
DB 2881 TATGTATGTCATGCCCGCAAAATATAGATGAAAGCATGTGAAGTGTCAAGTGTCAAGTGTCAATCC 2940
QY 2941 ATTTGATTTTTCATATTTGACACCGGAGAGTAGATACAAATACAAATGATAGTATTCATGT 3000
DB |||||
DB 2941 ATTTGATTTTTCATATTTGACACCGGAGAGTAGATACAAATACAAATGATAGTATTCATGT 3000
QY 3001 CTTTATTTAAATTTCTTAATCCAGATGGATCGCTACAGTAGGGAATCTAGAGTCAATTTGA 3060
DB |||||
DB 3001 CTTTATTTAAATTTCTTAATCCAGATGGATCGCTACAGTAGGGAATCTAGAGTCAATTTGA 3060
QY 3061 AGAAGGACCTAACAGGTGAAGCATTTGGCACAATGTGAAACAAAGGAAAGAAATGGAA 3120
DB |||||
DB 3061 AGAAGGACCTAACAGGTGAAGCATTTGGCACAATGTGAAACAAAGGAAAGAAATGGAA 3120
QY 3121 ACAACATGAGGAAAGAAAGCTTTGGGAAACACAAAGCCTATGATCCAGCAAAACAGGC 3180
DB |||||
DB 3121 ACAACATGAGGAAAGAAAGCTTTGGGAAACACAAAGCCTATGATCCAGCAAAACAGGC 3180
QY 3181 TGTAGATGCAATTTTACAAATGAAAGAGTTTACACTATCATATTTTACATATTTAGATCATAT 3240
DB |||||
DB 3181 TGTAGATGCAATTTTACAAATGAAAGAGTTTACACTATCATATTTTACATATTTAGATCATAT 3240
QY 3241 TCAAAAACGCTGATCGATCGTACAGTCCGATTCCTATGTATACATAATTTGGTTACCGAA 3300
DB |||||
DB 3241 TCAAAAACGCTGATCGATCGTACAGTCCGATTCCTATGTATACATAATTTGGTTACCGAA 3300
QY 3301 TGCTCCAGGTATGAACTATGATGTATTAAGAGTTTAAAGCAGCTATCATGTCAGAGGTTA 3360
DB |||||
DB 3301 TGCTCCAGGTATGAACTATGATGTATTAAGAGTTTAAAGCAGCTATCATGTCAGAGGTTA 3360
QY 3361 TAATTTTATATGATGACGAAATGTCATAACAAATGGTGTATTTACACAGGATTTACAGGG 3420
DB |||||
DB 3361 TAATTTTATATGATGACGAAATGTCATAACAAATGGTGTATTTACACAGGATTTACAGGG 3420
QY 3421 ATGGCAGCAACAGGAAATGCGCGGTACAAATGGATGGAGCTTCAGTATTAAGTTCT 3480
DB |||||
DB 3421 ATGGCAGCAACAGGAAATGCGCGGTACAAATGGATGGAGCTTCAGTATTAAGTTCT 3480
QY 3481 ATCAAAATGAGCGCGGGGTATCTCAAACTTGTGATGCTCAAGATCATCATGGATATGT 3540
DB |||||
DB 3481 ATCAAAATGAGCGCGGGGTATCTCAAACTTGTGATGCTCAAGATCATCATGGATATGT 3540

QY 3541 GTTACGTGTGATTGCCCCAAAAGAGGACTGCGAAAAGGGTATGTAAACGATGATGATTG 3600
DB |||||
DB 3541 GTTACGTGTGATTGCCCCAAAAGAGGACTGCGAAAAGGGTATGTAAACGATGATGATTG 3600
QY 3601 TAATGAAAAGCAGGAAACACTTTAAGTTCACTTCTTCCGGAAGAGGATATATGACAAAAC 3660
DB |||||
DB 3601 TAATGAAAAGCAGGAAACACTTTAAGTTCACTTCTTCCGGAAGAGGATATATGACAAAAC 3660
QY 3661 AGTAGAGGTTATTTCCCAAGAAAGTATCGTACGGATTGAAATAGGAGAAACCGAAGGTAC 3720
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QY 3721 ATTTTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGATATGATAACAAATTAACCT 3780
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QY 3781 GCACACGGGTAAATATATATGAGCAAAAGTTTATAATGGAATTTAATCAAAATTAAGCTAGCGA 3840
DB |||||
DB 3781 GCACACGGGTAAATATATGAGCAAAAGTTTATAATGGAATTTAATCAAAATTAAGCTAGCGA 3840
QY 3841 TGTGTATTTACCAAGGGTATACAAACAACTATTAACCAAGACTCTAGTAAATATGATTAATCA 3900
DB |||||
DB 3841 TGTGTATTTACCAAGGGTATACAAACAACTATTAACCAAGACTCTAGTAAATATGATTAATCA 3900
QY 3901 AAATTAATCTAAACATGATGACCTGCATTTCCGTTTCACATGTAACCAAGGGCATTAATC 3960
DB |||||
DB 3901 AAATTAATCTAAACATGATGACCTGCATTTCCGTTTCACATGTAACCAAGGGCATTAATC 3960
QY 3961 TGGCTGTACATGTATCAAGGATATTAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020
DB |||||
DB 3961 TGGCTGTACATGTATCAAGGATATTAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020
QY 4021 TGGGAAAATTAACCACTACTCACAATACTATTTCATATCATATCATTAACGCTTTTACAAA 4080
DB |||||
DB 4021 TGGGAAAATTAACCACTACTCACAATACTATTTCATATCATATCATTAACGCTTTTACAAA 4080
QY 4081 TAAACGACATATTTCTAGAAGAGTCTCTTAAATCTTAAATTAAGAGAGATTTTTCGTTT 4140
DB |||||
DB 4081 TAAACGACATATTTCTAGAAGAGTCTCTTAAATCTTAAATTAAGAGAGATTTTTCGTTT 4140
QY 4141 CCCCATAATTTGATTAATGAAAATTAATCTTTTACAGAAAGATTTTAGGCTGATTTGGTGT 4200
DB |||||
DB 4141 CCCCATAATTTGATTAATGAAAATTAATCTTTTACAGAAAGATTTTAGGCTGATTTGGTGT 4200
QY 4201 GTGCAAGCAGCAATTTCTGAAAATTCAGAAAAATTCAGAGGCAATGAGCTACTTTT 4260
DB |||||
DB 4201 GTGCAAGCAGCAATTTCTGAAAATTCAGAAAAATTCAGAGGCAATGAGCTACTTTT 4260
QY 4261 TAAATGTTTAAATTTGGTATTTCCAGAAAGATAAGGATTTTCGTAACGATAACTTTTCCACT 4320
DB |||||
DB 4261 TAAATGTTTAAATTTGGTATTTCCAGAAAGATAAGGATTTTCGTAACGATAACTTTTCCACT 4320
QY 4321 GTGAATGCAATGATATGAGCATGAGCAACAAACGGTCCCAACATGAGAGGTAAGCCCG 4380
DB |||||
DB 4321 GTGAATGCAATGATATGAGCATGAGCAACAAACGGTCCCAACATGAGAGGTAAGCCCG 4380
QY 4381 TTATCAACCAATATATACGATTCATTCAGCAACCAATTTCTAGTTTGAAGTAACTATGACACT 4440
DB |||||
DB 4381 TTATCAACCAATATATACGATTCATTCAGCAACCAATTTCTAGTTTGAAGTAACTATGACACT 4440
QY 4441 TTTTGTTCGTAAACAGTCGGCAATTAATGAAATAGGAGTCCGCTCTCTTGTCTTTGAAAT 4500
DB |||||
DB 4441 TTTTGTTCGTAAACAGTCGGCAATTAATGAAATAGGAGTCCGCTCTCTTGTCTTTGAAAT 4500
QY 4501 GGTACATAACCTAGTTTCACTAAAAATTAATAATCAAGGCTTCAATTTGCTTCTTTGATG 4560
DB |||||
DB 4501 GGTACATAACCTAGTTTCACTAAAAATTAATAATCAAGGCTTCAATTTGCTTCTTTGATG 4560
QY 4561 CGGGTTAAATTCCTTGTGTTTAAAGCTCTTCTTAATAGACCTACTAAATCTGCTACTCGG 4620
DB |||||
DB 4561 CGGGTTAAATTCCTTGTGTTTAAAGCTCTTCTTAATAGACCTACTAAATCTGCTACTCGG 4620
QY 4621 AAAAATTCCTTGTGATATCCCTGTTTCAAGCTTCAACCTTAATGCTGTAGCTAAATGT 4680

Db 301 TCTATATGTGATTTATTATCTATTAATTCGTAAGAGGAGGTAGCCGATAGTGTGTTTAAAGTCA 360
Qy 528 GCGATTTGAGATTTTTCGCGTAAATTCGAAATTTATAGAGAGTATTATCTTTCTTATCTT 587
Db 361 GCGATTTGAGATTTTTCGCGTAAATTCGAAATTTATAGAGAGTATTATCTTTCTTATCTT 420
Qy 588 GGGCTTTGGCTTAAAGACGCTAAACCACTTCAAAAGACAAATAATTCGATATCGGACAA 647
Db 421 GGGCTTTGGCTTAAAGACGCTAAACCACTTCAAAAGACAAATAATTCGATATCGGACAA 480
Qy 648 TTAGTTTATTTTAACTTTTCAAGAGAGATTTCAATGAAATTCAGAGGGTCAATTG 707
Db 481 TTAGTTTATTTTAACTTTTCAAGAGAGATTTCAATGAAATTCAGAGGGTCAATTG 540
Qy 708 TCAAGAAACCAATGCTCAAGTATTCGTTATCTACTCTTTTGCACAAAGCTGCAAAATGTGCAG 767
Db 541 TCAGAAACCAATGCTCAAGTATTCGTTATCTACTCTTTTGCACAAAGCTGCAAAATGTGCAG 600
Qy 768 TTATTACTATTAAGGGATGCAAGTTCAATATAAAGCACAAATGGTCCCAATTTTGGAGTGCA 827
Db 601 TTATTACTATTAAGGGATGCAAGTTCAATATAAAGCACAAATGGTCCCAATTTTGGAGTGCA 660
Qy 828 GAGAAATGAGATCGGAATTAATATACCTTAAACAGTGGTGTGATTTTACCGGTGATTAC 887
Db 661 GAGAAATGAGATCGGAATTAATATACCTTAAACAGTGGTGTGATTTTACCGGTGATTAC 720
Qy 888 TATGAGCGATTTAAATGCAAAACGCGAGAGTATACCAATTTATGTTTATATGTTATCTGATCAG 947
Db 721 TATGAGCGATTTAAATGCAAAACGCGAGAGTATACCAATTTATGTTTATATGTTATCTGATCAG 780
Qy 948 GTAGGTTTAAATCAGATAAAGACGGGGGACAGGCTGCTGACACTTCGGTCGAAATTTAAT 1007
Db 781 GTAGGTTTAAATCAGATAAAGACGGGGGACAGGCTGCTGACACTTCGGTCGAAATTTAAT 840
Qy 1008 AATTTTCGTAGAGAAATGAGCTTGGCGGTATGGAATATATGCTATATTTCAACTTAT 1067
Db 841 AATTTTCGTAGAGAAATGAGCTTGGCGGTATGGAATATATGCTATATTTCAACTTAT 900
Qy 1068 GATTTTCAGAGAAATTCATTCGGAACCTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 1127
Db 901 GATTTTCAGAGAAATTCATTCGGAACCTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 960
Qy 1128 GCAAGTGGATTTTCAATCGGAACCTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 1187
Db 961 GCAAGTGGATTTTCAATCGGAACCTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 1020
Qy 1188 GGGTTAGAGCTTAATGGAACACGGGGACCTGGTTTATGTTACTGGCTTAGCAAAATAGGT 1247
Db 1021 GGGTTAGAGCTTAATGGAACACGGGGACCTGGTTTATGTTACTGGCTTAGCAAAATAGGT 1080
Qy 1248 ATATATAATCAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTCGCTATTATGAA 1307
Db 1081 ATATATAATCAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTCGCTATTATGAA 1140
Qy 1308 GACTACACAAAGGGTAAACGGTATTTTCAACGATATGTTCTGGAACCTACGAGTAATGATCTA 1367
Db 1141 GACTACACAAAGGGTAAACGGTATTTTCAACGATATGTTCTGGAACCTACGAGTAATGATCTA 1200
Qy 1368 CGTAATATGATTTTCAAGATGCGGATGATATAAATAATTAATTAATTAATTAATTAATTAATTA 1427
Db 1201 CGTAATATGATTTTCAAGATGCGGATGATATAAATAATTAATTAATTAATTAATTAATTAATTA 1260
Qy 1428 CTAGTAGGAGACTACCGCTAGACAGATGCTGTTTCAAGGGCAGATTTTTCGTAGG 1487
Db 1261 CTAGTAGGAGACTACCGCTAGACAGATGCTGTTTCAAGGGCAGATTTTTCGTAGG 1320
Qy 1488 GTAGGGGACCTGATTTTAAATTTATGATGCAAGTAAATGGGCTTAAGCAGGATGCAAAAT 1547
Db 1321 GTAGGGGACCTGATTTTAAATTTATGATGCAAGTAAATGGGCTTAAGCAGGATGCAAAAT 1380
Qy 1548 GAATCTACGTTCCGCTGATTTGCTACTTAATGGTGTAGAGACCTCTCATAGATTA 1607
Db 1381 GAATCTACGTTCCGCTGATTTGCTACTTAATGGTGTAGAGACCTCTCATAGATTA 1440

Qy 1608 TCAAAATCGCGCATGTTGTATATGGAACCTCCAGAGTTAAACGTATATGTTGGACACAT 1667
Db 1441 TCAAAATCGCGCATGTTGTATATGGAACCTCCAGAGTTAAACGTATATGTTGGACACAT 1500
Qy 1668 ACAAGTTTAAACCGTGAATAATAATTAAGAACCAATCAAAATTAACAAAATACCCGCGGTG 1727
Db 1501 ACAAGTTTAAACCGTGAATAATAATTAAGAACCAATCAAAATTAACAAAATACCCGCGGTG 1560
Qy 1728 AAGAGTTTATACCTTCAAAATTTATCTGCTTAATGCTTATACCTATGCTATGTAATAAAGGCACT 1787
Db 1561 AAGAGTTTATACCTTCAAAATTTATCTGCTTAATGCTTATACCTATGCTATGTAATAAAGGCACT 1620
Qy 1788 CATACAGTGGCGGATTTAATCCGTTTAAAGAACCAAAATCAGAGTATAACGCAAGTTTAT 1847
Db 1621 CATACAGTGGCGGATTTAATCCGTTTAAAGAACCAAAATCAGAGTATAACGCAAGTTTAT 1680
Qy 1848 GCAGGTGGCGGAATTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTATT 1907
Db 1681 GCAGGTGGCGGAATTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTATT 1740
Qy 1908 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGT 1967
Db 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGT 1800
Qy 1968 TGGGGTTCAAAATCGTTTGTATCGCTTGAAGAAATCTTACTCTGGAATTTATGAGATTTA 2027
Db 1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAAGAAATCTTACTCTGGAATTTATGAGATTTA 1860
Qy 2028 AAATATAGTGAATTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAACATT 2087
Db 1861 AAATATAGTGAATTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAACATT 1920
Qy 2088 CAGATGATGTGAGATGCAAGCGAATAGTTTTCATTCAGATGTAACGTGGTTCTCGAC 2147
Db 1921 CAGATGATGTGAGATGCAAGCGAATAGTTTTCATTCAGATGTAACGTGGTTCTCGAC 1980
Qy 2148 AAAATTTGAATTCCTCCCAAGTAAATACAAACCTTTAGAAATATGAGGAGAACCGGACCTA 2207
Db 1981 AAAATTTGAATTCCTCCCAAGTAAATACAAACCTTTAGAAATATGAGGAGAACCGGACCTA 2040
Qy 2208 GAAAAACAAAGAACCGGCTGAACGATCTGTTTACCAATTA 2249
Db 2041 GAAAAACAAAGAACCGGCTGAACGATCTGTTTACCAATTA 2082

RESULT 3

US-10-781-979-4
; Sequence 4, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCES: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2073)
US-10-781-979-4

Query Match		34.7%	Score 2073;	DB 8;	Length 2073;	
Best Local Similarity		100.0%	Pred. No. 0;			
Matches 2073;		Conservative	0;	Mismatches	0;	Indels 0;
					Gaps	0;
Qy	177	ATGAGTCCATATCAAAATATAAATGAATATGAATATGAAATATTTGGAATCCTCATCGAATAACACA	236			
Db	1	ATGAGTCCATATCAAAATATAAATGAATATGAAATATTTGGAATCCTCATCGAATAACACA	60			
Qy	237	AATACGCCAAACAGATATCCTTTTGCAGATATAATCGGGATATGCTACTATGCTTCGGAAT	296			
Db	61	AATACGCCAAACAGATATCCTTTTGCAGATATAATCGGGATATGCTACTATGCTTCGGAAT	120			
Qy	297	GATTTGTCAGGGAATCTCATGGATGAATTTTGGGAATCAGTCGAAACGATAACAAGTATT	356			
Db	121	GATTTGTCAGGGAATCTCATGGATGAATTTTGGGAATCAGTCGAAACGATAACAAGTATT	180			
Qy	357	GGGATAAATCTTATAGAGTTTGTGATAGAACCTTAGTTTGGGTGGGAATTAATACACTATT	416			
Db	181	GGGATAAATCTTATAGAGTTTGTGATAGAACCTTAGTTTGGGTGGGAATTAATACACTATT	240			
Qy	417	TCAATTAATAGGAAACCTAATTCGCACTTAATCGTCAAACTGTGTACGACCTTTCTATATGT	476			
Db	241	TCATTAATAGGAAACCTAATTCGCACTTAATCGTCAAACTGTGTACGACCTTTCTATATGT	300			
Qy	477	GATTTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAAGTGATCGATTGCA	536			
Db	301	GATTTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAAGTGATCGATTGCA	360			
Qy	537	GATTTTGACGGTAAATGAAATTAATAGAGATATATCTTCTTATCTTGGGGCTTGG	596			
Db	361	GATTTTGACGGTAAATGAAATTAATAGAGATATATCTTCTTATCTTGGGGCTTGG	420			
Qy	597	CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGACAAATTAGTTTAT	656			
Db	421	CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGACAAATTAGTTTAT	480			
Qy	657	TATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCATTTGTCAGAAAC	716			
Db	481	TATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCATTTGTCAGAAAC	540			
Qy	717	ATGCTCAAGTATGTTATACCTACTTTTGCAGAGCTGCAATGTCAGTTTACTA	776			
Db	541	AATGCTCAAGTATGTTATACCTACTTTTGCAGAGCTGCAATGTCAGTTTACTA	600			
Qy	777	TTAAGGGATGCAGTTCAAATATAAGCACAAATGCTCCCATTTTGTAGTGCAGAGAATGTA	836			
Db	601	TTAAGGGATGCAGTTCNAATATAAGCANAATGGTCCCATTTTGTAGTGCAGAGAATGTA	660			
Qy	837	AGATCGGAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGA	896			
Db	661	AGATCGGAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGA	720			
Qy	897	TTAABATGCAAAACGGCAGATATACCAATATGTTTATATGTTATGTTATCAGGTAGTTTA	956			
Db	721	TTAABATGCAAAACGGCAGATATACCAATATGTTTATATGTTTATGTTATCAGGTAGTTTA	780			
Qy	957	AATCAGATATAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAATAAATTTTCTG	1016			
Db	781	AATCAGATATAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAATAAATTTTCTG	840			
Qy	1017	AGAGAAATGAGTGGCGGTATTTGGATATPATCGCTATATTTCCAACTTATGATTTTGAG	1076			
Db	841	AGAGAAATGAGTGGCGGTATTTGGATATPATCGCTATATTTCCAACTTATGATTTTGAG	900			
Qy	1077	AAATATCCATTGCCAACACATGTAGAGTTGACCTAGGGAAATTTATACAGATCAGTGGGA	1136			
Db	901	AAATATCCATTGCCAACACATGTAGAGTTGACCTAGGGAAATTTATACAGATCAGTGGGA	960			
Qy	1137	TATTCATCGGGAACTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAATGGGTTAGAG	1196			
Db	961	TATTCATCGGGAACTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAATGGGTTAGAG	1020			

Qy	1197	GCTAATGGAACACCGGGACCTGGTTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT	1256
Db	1021	GCTAATGGAACACCGGGACCTGGTTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT	1080
Qy	1257	GAGTATGTTTCGAGATATTTTCCCGCTGGGTAGGAATCTCGTCATATGAAGACTACACA	1316
Db	1081	GAGTATGTTTCGAGATATTTTCCCGCTGGGTAGGAATCTCGTCATATGAAGACTACACA	1140
Qy	1317	AAGGGTAAACGGTATTTTCAACGTATGCTCGAACTACGAGTAATGATCTACGTAATATT	1376
Db	1141	AAGGGTAAACGGTATTTTCAACGTATGCTCGAACTACGAGTAATGATCTACGTAATATT	1200
Qy	1377	GATTTTCAGAAATGCGGATGATATAAATAATTAATCTTCAATGATGATCATGAACCTAGTAGA	1436
Db	1201	GATTTTCAGAAATGCGGATGATATAAATAATTAATCTTCAATGATGATCATGAACCTAGTAGA	1260
Qy	1437	GAGACTACCGCTAGACACGAGTATCGTGTCTTCAAGGCGAGATTTTTCGTAGGGTAGGGGA	1496
Db	1261	GAGACTACCGCTAGACACGAGTATCGTGTCTTCAAGGCGAGATTTTTCGTAGGGTAGGGGA	1320
Qy	1497	CCTGATTTAAATATATGATGCGAGTAAATATGCGCTAAGCAGGATGACAAATGAAATCTAG	1556
Db	1321	CCTGATTTAAATATATGATGCGAGTAAATATGCGCTAAGCAGGATGACAAATGAAATCTAG	1380
Qy	1557	TTCCCACTTTGATGCGACTCTAATGGGTAGAGGACCTCTCATAGATTATCAAAATGCG	1616
Db	1381	TTCCCACTTTGATGCGACTCTAATGGGTAGAGGACCTCTCATAGATTATCAAAATGCG	1440
Qy	1617	GCATGTTGTATATGGAACCTCCAGAGTTAACGTTATATGTTGGACACATACAGTTTA	1676
Db	1441	GCATGTTGTATATGGAACCTCCAGAGTTAACGTTATATGTTGGACACATACAGTTTA	1500
Qy	1677	AAACGTGAAAATATTAATTAAGGCCAATCAAAATTAACAATAACCGCGGTGAAGATTAT	1736
Db	1501	AAACGTGAAAATATTAATTAAGGCCAATCAAAATTAACAATAACCGCGGTGAAGATTAT	1560
Qy	1737	TACCTTCAAAATTTCTTGCTAATGCTATACCTATGTAATAAAGGCCATCATACAGGT	1796
Db	1561	TACCTTCAAAATTTCTTGCTAATGCTATACCTATGTAATAAAGGCCATCATACAGGT	1620
Qy	1797	GGGGATTTAATCCGTTTTTAAAGAACAAATCAGAGTATAACGAGTTTATCGAGTGGC	1856
Db	1621	GGGGATTTAATCCGTTTTTAAAGAACAAATCAGAGTATAACGAGTTTATCGAGTGGC	1680
Qy	1857	GGAAATGATGATTATTAATAACAAAACCTGCAGGACAAAGTTACCGTATTCGTTTCGT	1916
Db	1681	GGAAATGATGATTATTAATAACAAAACCTGCAGGACAAAGTTACCGTATTCGTTTCGT	1740
Qy	1917	TATGCTGCAGATAAAGTGTCTTTTATGTTATATCTTTATCCAGGAGGTGGGGTTCA	1976
Db	1741	TATGCTGCAGATAAAGTGTCTTTTATGTTATATCTTTATCCAGGAGGTGGGGTTCA	1800
Qy	1977	AATCGTTTTGTATCGCTGAAAATCTTACTCTGAAAATTAATGACGATTTTAAATATAGT	2036
Db	1801	AATCGTTTTGTATCGCTGAAAATCTTACTCTGAAAATTAATGACGATTTTAAATATAGT	1860
Qy	2037	GATTTTAAATTCGCTGAAATTTATCACCTCCATTAACCTAGTTTCAAAACATTCAGATGGAT	2096
Db	1861	GATTTTAAATTCGCTGAAATTTATCACCTCCATTAACCTAGTTTCAAAACATTCAGATGGAT	1920
Qy	2097	GTGGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACCGTGGTTCTCGACAAATTTGAA	2156
Db	1921	GTGGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACCGTGGTTCTCGACAAATTTGAA	1980
Qy	2157	TTCTCTCCCAAGTAATAACAACAACTTTAGAAATAGGGGAGAACGGGACCTAGAAAAACA	2216
Db	1981	TTCTCTCCCAAGTAATAACAACAACTTTAGAAATAGGGGAGAACGGGACCTAGAAAAACA	2040
Qy	2217	AAGAAACGGGTGAACGATCTGTTTACCAATTAA	2249
Db	2041	AAGAAACGGGTGAACGATCTGTTTACCAATTAA	2073

RESULT 4

US-10-781-979-6

; Sequence 6, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargies, Tracy

; APPLICANT: Koziel, Michael G.

; APPLICANT: Duck, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and

; FILE OF INVENTION: Methods for Its Use

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10781.979

; CURRENT FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,797

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 1686

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1686)

US-10-781-979-6.

Query Match

Best Local Similarity 100.0%; Score 1686; DB 8; Length 1686;

Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2309	GTGAGTCCTATGTTTACAACTAGTACGAAATACGTTAAATATAGAAACGACAGATTAT	2368
DB	1	GTGAGTCCTATGTTTACAACTAGTACGAAATACGTTAAATATAGAAACGACAGATTAT	60
QY	2369	GAATAGATCAAGCGGCATTTCTATAGATGTTATGTCAGATGAAACAAATCTCAGGAA	2428
DB	61	GAATAGATCAAGCGGCATTTCTATAGATGTTATGTCAGATGAAACAAATCTCAGGAA	120
QY	2429	AAATATGTTATGGATGAAATATAAATCGGCAAAACAACTTAGTCAGTCTCGTAATCTA	2488
DB	121	AAATATGTTATGGATGAAATATAAATCGGCAAAACAACTTAGTCAGTCTCGTAATCTA	180
QY	2489	CTCCAAATCGAGACTTTCTGGGAATGATTGGACATTCGGTAATGATATATATAGGA	2548
DB	181	CTCCAAATCGAGACTTTCTGGGAATGATTGGACATTCGGTAATGATATATATAGGA	240
QY	2549	TCCAATAATCCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGAGACATATAT	2608
DB	241	TCCAATAATCCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGAGACATATAT	300
QY	2609	GGAACTCTATTTCCAACTTATATCTGTCAAAATATAGATGAGTCTAAATTTAAACCATAT	2668
DB	301	GGAACTCTATTTCCAACTTATATCTGTCAAAATATAGATGAGTCTAAATTTAAACCATAT	360
QY	2669	ACAGTTATCGAGTACAGGGTTTGGGAAGTAGTAAGATTTGAAATTTAATGGTAACA	2728
DB	361	ACAGTTATCGAGTACAGGGTTTGGGAAGTAGTAAGATTTGAAATTTAATGGTAACA	420
QY	2729	CGTTACGGGAAAGAAATTTGATGCTATCATGAAATGTTCCAAATGATTTGGCCTATATGCAG	2788
DB	421	CGTTACGGGAAAGAAATTTGATGCTATCATGAAATGTTCCAAATGATTTGGCCTATATGCAG	480
QY	2789	CCTAAATCCTTATGTTGAGATTAATCGCTGTAATCATCGTCTCAGTATGTGAGCCAAAGG	2848
DB	481	CCTAAATCCTTATGTTGAGATTAATCGCTGTAATCATCGTCTCAGTATGTGAGCCAAAGG	540
QY	2849	TATCCTACACCAACAGATGATGTCCTCGATATGTTATGTCATGCCGCAAAATATAGAT	2908
DB	541	TATCCTACACCAACAGATGATGTCCTCGATATGTTATGTCATGCCGCAAAATATAGAT	600
QY	2909	AGAAAGCATGTGAAGTGTACAGATCGTCATCCATTTTTCATATTTGACACCGGAGAA	2968

DB	601	AGAAAGCATGTGAAGTGTACAGATCGTCATCCATTTGATTTTCATATTTGACACCGGAGAA	660
QY	2969	GTAGATACAAATACAAATGTAGTATGTCTTATTTAAATTTCTAATCAGATGGA	3028
DB	661	GTAGATACAAATACAAATGTAGTATGTCTTATTTAAATTTCTAATCAGATGGA	720
QY	3029	TACGCTACAGTAGGGAACTTAGAAGTCATTGAGAGAGGACCCTACAGGTGAGCAATG	3088
DB	721	TACGCTACAGTAGGGAACTTAGAAGTCATTGAGAGAGGACCCTACAGGTGAGCAATG	780
QY	3089	GCACATGTGAAAACAAAGGAAATGAAAACAAACACATGAGAGAAAAACCTTGGGAA	3148
DB	781	GCACATGTGAAAACAAAGGAAATGAAAACAAACACATGAGAGAAAAACCTTGGGAA	840
QY	3149	ACAAACAAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCTATTTTACAAATGAACAA	3208
DB	841	ACAAACAAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCTATTTTACAAATGAACAA	900
QY	3209	GAGTTACACTATCATATTTACTTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTCG	3268
DB	901	GAGTTACACTATCATATTTACTTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTCG	960
QY	3269	ATTCCCTATGTATACCATTAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGATAT	3328
DB	961	ATTCCCTATGTATACCATTAATTGGTTACCGAATGCTCCAGGTATGAACTATGATGATAT	1020
QY	3329	CAAGAGTTAAACGCGATCATGCAAGGTTATTAATTTATATGATGACGAAATGTCATA	3388
DB	1021	CAAGAGTTAAACGCGATCATGCAAGGTTATTAATTTATATGATGACGAAATGTCATA	1080
QY	3389	ACAAATGTTGACTTTTACAAAGGATTCAGGGATGCGACGACAGGAAATGCCGGGTA	3448
DB	1081	ACAAATGTTGACTTTTACAAAGGATTCAGGGATGCGACGACAGGAAATGCCGGGTA	1140
QY	3449	CAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAAATGGAGCGCGGGGTATCTCAA	3508
DB	1141	CAACAAATGGATGGAGCTTCAGTATTAGTTCTATCAAAATGGAGCGCGGGGTATCTCAA	1200
QY	3509	AACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTCGCCAAAAAGAGGA	3568
DB	1201	AACTTGCATGCTCAAGATCATCATGGATATGTGTTACGTGTGATTCGCCAAAAAGAGGA	1260
QY	3569	CTTGGAAGAGGTGTGTAACGATGATGTTGTTGTAAGAGGAGGAGGAAACACTTAAGTTC	3628
DB	1261	CTTGGAAGAGGTGTGTAACGATGATGTTGTTGTAAGAGGAGGAGGAAACACTTAAGTTC	1320
QY	3629	ACTTCTTGGGAAAGAGGATATATGCAAAACAGTAGAGGTATTTCCAGAAAGTGTATCGT	3688
DB	1321	ACTTCTTGGGAAAGAGGATATATGCAAAACAGTAGAGGTATTTCCAGAAAGTGTATCGT	1380
QY	3689	GTACGGATTTGAAATAGGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTT	3748
DB	1381	GTACGGATTTGAAATAGGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTT	1440
QY	3749	TGTTATGCAAGGATATGATTAACAAATTAATACCTGCAACCGGTAATATGTTATGAGCAAGT	3808
DB	1441	TGTTATGCAAGGATATGATTAACAAATTAATACCTGCAACCGGTAATATGTTATGAGCAAGT	1500
QY	3809	TATAATGGAATTTAATAATCAAAATCTAGCGATGTGTTATACCAAGGGTATACAAACAAC	3868
DB	1501	TATAATGGAATTTAATAATCAAAATCTAGCGATGTGTTATACCAAGGGTATACAAACAAC	1560
QY	3869	TATAACCAAGACTCTAGTATTAATGATTAATCAAAATTTATATCAAAATGATGACCTGCAT	3928
DB	1561	TATAACCAAGACTCTAGTATTAATGATTAATCAAAATTTATATCAAAATGATGACCTGCAT	1620
QY	3929	TCCGGTTGACATGTAAACCAAGGCGATACCTCTGGCTGTACATGTTAATCAAGGATATAC	3988
DB	1621	TCCGGTTGACATGTAAACCAAGGCGATACCTCTGGCTGTACATGTTAATCAAGGATATAC	1680
QY	3989	CGTTAA 3994	


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US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-141-1

Query Match      14.3%; Score 855; DB 8; Length 2145;
Best Local Similarity 71.4%; Pred. No. 5.5e-169;
Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

QY 49 AAATAATGGGTTATTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATAT 108
DB 8 AAATAATAATGTTTTTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATAT 67

QY 109 ATAGAAAGACACCTAACATATATTTTAGTGTCTTAAATAAAGACCTATATATAGGAG 168
DB 68 ATAGAAAGACACCTGGCATATATTTTAGTGTCTTAAATAAAGACCTATATATAGGAG 127

QY 169 TGAATAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAACTCTCATCGA 228
DB 128 TGAATAATAATGAATCTTATCAAAATAAATAAATGAATATGAATATTTGGATGGTTCCCGA 187

QY 229 ATACACAAATAGCCMAACAGATATCTTTTGGAAATAATTCGGGATATGCTACTATGT 288
DB 188 ATACACAAATATGTCAACAGATATCTTTTGGAAAGATCAAAATATATTTTCTTATTA 247

QY 289 CTTGGATGATTTGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA 348
DB 248 ACCTGGACGCTTGTGAGGAAGCCATGGCAAGATACGTGGGAATCAGTCTCGATATAG 307

QY 349 CAAGTATGGGATAAATCTTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATA 408
DB 308 TAAGTATGGGACATACCTTATACAAATCTTGTAGNACCCTGATAGGTGGAAATTCCTG 367

QY 409 CACTATTAATCAATAAGGAAACCTAATTCGCGCTAATTCGTCAAACTGTGTACGACTTT 468
DB 368 TAATAATTTTCAATAATAAACAACCTCAATTCGCTCTTGTGCTCAATCTGTGGCAGCACTT 427

QY 469 CTATATGATTTATTTATCTATATTCGTAAAGGCTAGCCGATAGTTTAAAGTATG 528
DB 428 CTATATGATTTATTTATCTATATTCGTAAAGGCTAGCCGATAGTTTAAAGTATG 487

QY 529 CGATTGCGATTTTGGCGTAAATTTGAAATAATTTATAGAGATATTTCTTCTTATCTTG 588
DB 488 GGGTTCGATTTTGGGGTGAATGCTCTTATCAAGATATTTATCTTATATCTTCTTG 547

QY 589 GGGCTTGGCTTAAGACGGTAAACCTTCAAAAGACAAATAATCTGTATATCGGCAAT 648
DB 548 AGGATTTGGCTTACAG-----ATAAATCAAAATCTTAAATAAATTTGCTGAGC 592

QY 649 TAGTTTATTTATTTAACTTTCAAGAGATTTCAATGAATTTCTAGAGGGTCAATGT 708
DB 593 TAGTTAAACAGTTCCCAAGCAGCGGAAGATTTCACTAACTTTTACAGGGGTCAATAT 652

QY 709 CAAGAAACAAATGCTCAAGTATTTGTTATACCTACTTTTGCACAAAGCTGCAAAATGTGAGT 768

653 CAAGACAGAAAGCTGAAATATTTATTTAGCTTACGTATGTGCAAGCTGCAAAATGTGCAAT 712
769 TATTACTATTAAGGGATGCAAGTTCAATATATAAGACAAATGGTTCCCATTTTGGAGTGCAG 828
713 TATTACTATTAAGGGACGCAAGTTAAATATAAAAAAGAAATGGGAGTGTGTGTCACCGT 772
829 AGAATGTAGATCGGAATTAATATACCTAACAGTGGTTGTGATTTTACCGGTGATTTACT 808
773 TGTATCCAGGTCAGGAGAA-----CTGATTGTA 802
889 ATGAGCGATTTAAATGCAAAACGCGAGAGTATACCAATTTATTTTATTTGATATCAGG 948
803 ACAGCGGTTTAAAGCGAAATAAAAGAGTATATAATTTATTTGTTAGGTGCTGATAACA 862
949 TAGGTTTAAATCAGATATAAAACAGGGGGGACAGGTGCTGACACTTGGTGCATAATTAATA 1008
863 AGGGTTTATAGATCAGATTAAGACAGCGCGGTACAAAGTCTGAAAGTTTGGTCGAAATTAATA 922
1009 AATTTCTGAGAGAAATGACGTTTGGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTATG 1068
923 AATTTCTGAGAGAAATGACGTTTGGCGGTATTTGGATATTTATTTTCCAACTTATG 982
1069 AATTTGAGAAATATCCATTTGCCAAACATGTAGAGTTGACTAGGGAAATTTATACAGATG 1128
983 AATTTGAGAAATATCCATTTAGCAACAGGTAGAGTTAACTAGGGAAATTTATACAGATC 1042
1129 CAGTGGGATTTATCATCGGGAACCTTATAGTTGGTTACGGAATTTGGCCCTAATATCTTTTAATG 1188
1043 CAGTGGGATTTATCAGGGGAAATTTATGGTTGGGAACGGTTTT-----TTAGCTTTAAAT 1096
1189 GGTTAGAGCTAATGCAACACGCGGACCTGGTTTACTTACTTGGCTTAGCCAAATAGGTA 1248
1097 CGGTAGAGCAATGAACACGCGGACCTGGTTTACTTACTTGGCTTAGCCAAATAGGTA 1156
1249 TATATATGAGTATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGAACTCGTC 1299
1157 TATATAGTCACTCTATTATTTTACGTTGGTTATCTTAGTGGCTGGGGGAACTCGTC 1216
1300 ATTATGAAGACTACACAAAGGGTAAAGGTTATTTTCAACGATATGTCTGGAATACAGATG 1359
1217 ATTATGAAGACTTCAAAAGGGTAAAGGTTATTTTCAACGATATGTCTGGAATACAGATG 1276
1360 ATGATCTAGTAAATTTGATTTTTCAGAAATGCGGATGATATATAAATTTACTTCAATAGCTA 1419
1277 ATAATCCAGTAAATATTTTGGCAATACCGGATATTTTAAATTTATTTTCAATAGCTA 1336
1420 TCATG---AACCTAGTAGGAGAGACTACCGCTAGACAGAGTATCTGTGTTTCAAGGCGAG 1476
1337 GATATGCAATGCAACCGTTTGTGGGTATTTCAATCCACGGCATCTTGTTCACGTGCGAG 1396
1477 ATTTTCGTAGGGTAGGGGACCTGATTTAAATTTATGATGAGGTAAATAATGGGCTAAGCA 1536
1397 AATTTTTCGCAACACACTAAATTTCTCTGATGAGGTAAACAGTCTCTGGGTA---CT 1453
1537 GGATGCAATTCGAATCTAGCTTCCACCTTGTATTTGACCTCTAA-----TGGTGTAGAG 1590
1454 CACAGCAATTAATGATCTGTTTACAGGTATTAATAAGGATCTACCACTAGTCTGACAA 1513
1591 GACCTCTCATAGATTTATCAAAATGGGCAATGTTGTATATGGAATCTCAGAGTTTAAAG 1650
1514 ATTACTCTCATAGATTTCAATTTGGGCAATGTTTCAAAATGAACCTCAGAGTTTAAAG 1573
1651 TATATGGTTGGACACATCAAGTTTAAAGAGTGAATAATAATTTGAAGCCAAATCAAAATTA 1710
1574 TATTTGGTTGGACACATCAAGTATGAAAAAAGATAATCGAATTTTATCCAGATAAAATTA 1633
1711 CACAAATACGGGGTGAAGATTTATCTTCAAAATTTATCTTGTCTAATGCTATACCT 1770
1634 CGAAATTCCTGAGTAAAGGCTTTTGGCTTACCAGCAGGTACAGGATATGCGAGGTT 1693
1771 ATGTAATAAAGGCACT 1787
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Db 1694 ACCTCAGCTGGGCCT 1710
RESULT 7
US-10-929-754-2
; Sequence 2, Application US/10929754
; Publication No. US20050124803A1
; GENERAL INFORMATION:
; APPLICANT: ABDULLAH, MODH AMIR
; APPLICANT: DEAN, DONALD H.
; TITLE OF INVENTION: INSECTICIDAL CRYSTAL PROTEINS WITH ENHANCED TOXICITY
; FILE REFERENCE: 22727/04179
; CURRENT APPLICATION NUMBER: US/10/929,754
; PRIOR FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: 60/498,826
; PRIOR FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-929-754-2
Query Match 13.2%; Score 789; DB 9; Length 3684;
Best Local Similarity 71.3%; Pred. No. 5.4e-155;
Matches 1092; Conservative 0; Mismatches 415; Indels 24; Gaps 3;
QY 2260 TTTACTAGAAATGGTGTATTGCTGTTTAAACAATAAGCGAAAAAGGTTGTGAGTCCTAT 2319
Db 2064 TGTATTAGATGACAGACAGAGAACCAAAATTTAGAAATCAGAACGAGAGATTGTGTAATGCACT 2123
QY 2320 GTTTACAAGTAGTACGAAAAAATACGTTTAAAAATAGAAAACGACAGATTATGAATAGATCA 2379
Db 2124 GTTTACAATAGCAGCGGAAAGATGCAATTAACATTTGGAACGACAGATTATGACATAGATCA 2183
QY 2380 AGCGGCCATTTCTATAGAAATGATGTCAGATGAACAAAAATCCTCAGGAAAAAATAATGTT 2439
Db 2184 AGCGGCAATCTTGTGGAAATGTTTCTGAAGAATTTATATCCAAAAAGAAAAATGCTGTT 2243
QY 2440 ATGGGATGAATAAACTGCAAAACAACTTAGTCAGTCTCGTAATCTACTCCAAAAATG 2499
Db 2244 ATTAGATGAAGTTTAAATGCGAAACAACTTAGTCAATCTCGAAATGTACTTCAAACCG 2303
QY 2500 AGACTTT-----TCTGGGAATGATTGGACATTCGGTAATGATATTATCATAGATCCAA 2553
Db 2304 GGATTTTGAATCGCTACGCTTGGTTGGCAACAAGTGATAATATCACAAATTCAGAAGA 2363
QY 2554 TATCTCTATTTTAAAGGAAAAATTTCTACAGATCGGTGGAGCAGACATATATGGAAC 2613
Db 2364 TGATCTCTATTTTAAAGGGCAATTAACCTTCATATGTCTGGGGCGAGAGACATTTGATGGTAC 2423
QY 2614 TCTATTTCACACTATATCTGCAAAAAATAGATGAGTCTPAAATTTAAACCATATACAG 2673
Db 2424 GATATTTCCACCTATATATCCAAAAATTTGATGAATCMAAATTTAAACCGTATACAG 2483
QY 2674 TTATCGAGTAAGAGGGTTTGTGGGAAAGTAGTAAAGATTTGAAATTAATGGTAAACAGTTA 2733
Db 2484 TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAGATGTAGAACTAGTGGTTTCACGCTA 2543
QY 2734 CGGGAAGAATTTGATGCTATCATGAAATGTTCCAAATGATTTGGCCTATATGAGCGCTAA 2793
Db 2544 TGGGGAAGAATTTGATGCCATCATGAATGTTCCAGCTGATTTTAAACTATCTGTATCTTTC 2603
QY 2794 TCCTTCATGTGGAGATTATCGCTGTGAATCATCTGTCAGTATGTGAGCCCAAGGGTATCC 2853
Db 2604 TAC-----CTTTGATTTGAGGGTCTAATCGTTGTGAGACGTCCTGCTGCC 2651
QY 2854 TACACCAACAGATGGATATGCTCCGATATGTATGATGCCCGCAAAATATAGATAGAAA 2913
Db 2652 GGCTAACATTTGGGAACACTTCTGATATGTTGTTATTCATGCCAATATGATACAGGAAAAA 2711
QY 2914 GCATGTGAAGTGTCCAGATCGTCATCCATTTGATTTTCATATTTGACACCCGGAGAGTAGA 2973
Db 2712 GCATGTGCTATGTCTAGGATCCCATCAATTTAGTTTCACTATTGATACAGGGGCATTAGA 2771
QY 2974 TACAAATACAAATGTAGGTATTGATGCTTATTAATAAATTTCTAATCCAGATGGATACGC 3033
Db 2772 TACAAATGAAATATATAGGGTTTGGGTCAATGTTTAAATATCTTCTCCAGATGGATACGC 2831
QY 3034 TACAGTAGGGAATCTAGAAAGTCATTTGAAGAAGGACCACTAAACAGGTGAAGCAATGGCACA 3093
Db 2832 ATCATTTAGATAATTTTGAAGTAATTTGAAGAGGGCCAAATAGATGGGAAGCACTGTGCAG 2891
QY 3094 TGTGAAACAAAGGAAAGAAATGAAACACACATGAGGAAAAAACCTTTGGGAAACACA 3153
Db 2892 CGTGAACACATGCGGAGAAAGAAATGGAACGATCAAAATGGAAGCAAAACGTTTCGGAACACA 2951
QY 3154 ACAAGCTATGATCCAGCAAAACAGGCTGTAGATCACTATTATTAACAATGAACAAGA--- 3210
Db 2952 ACAGCATATGATGTAGCGAAACAGCCATTTGATGCTTTATTCACAAATGTACAGATGA 3011
QY 3211 ---GTTACACTATCATATTTACTTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTC 3267
Db 3012 GGCTTTTACAGTTTGATACGACACTCGCTCAAATTCAGTACGCTGAGTATTTGGTCAAAATC 3071
QY 3268 GATTCCTCTATGTATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACATGATGATATA 3327
Db 3072 GATTCATATGTGTACAATGATTTGGTTGTCCAGATGTTCCAGGTATGAATTTATGATATCTA 3131
QY 3328 TCAAGAGTTAAACGACGCTATCATCAAGGTTTATAATTTATATGATGACACGAAATGTCTAT 3387
Db 3132 TGTAGATTGGATGACAGAGTGGCAAGCGGTTATTTGTATGATACAGAAATATTTAT 3191
QY 3388 AACAAATGGTGTATTTTACACAGGATTAACAGGATGCGCAACAGCAAGAAATGCGCGGT 3447
Db 3192 TAAAAATGGTGTATTTTACACAGGGTAAATGGGGTGGCATGTAACCTGGAATTCAGACGT 3251
QY 3448 ACAACAAATGGATGAGCTTCAGTATTAGTTCTATCAAAATTTGGAGCGGGGGGTATCTCA 3507
Db 3252 ACAACAAATAGATGTTGTTCTGTATTTGTTCTATCAATTTGGAGTGTGGCGGTATCTCA 3311
QY 3508 AAATCTGATGCTCAAGATCATCATGATATGTTGTAGTGTGATTTGCCAAAAAGAAAGG 3567
Db 3312 AAATGTCATCTCCAAACATATCATGGGTATGTTCTTACGTTATTTGCCAAAAAGNAGG 3371
QY 3568 ACCTGGAAGAGGTATGTAACGATGATGATGATGTAATGGAAGCAGGAAACAACCTTAAGTT 3627
Db 3372 ACCTGGAAGAGGTATGTCACGCTTATGGAATGTCAGGAGAAATCAAGAAAAATTCACGTT 3431
QY 3628 CACTTCTTCGGAAGAGGATATATACAAABACAGTACAGGTATTTCCAGAAAGTATCG 3687
Db 3432 TACGCTCTTGTGGAAGAGGATATATTACGAAGACAGTAGATGTTATTTCCAGATACAGATCG 3491
QY 3688 TGTACGGATTGAAATAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCT 3747
Db 3492 TGTACGAATTGAGATAGCGGAACCGAAGGTTCGTTTTATATCGAAAGCATTTGAATTAAT 3551
QY 3748 TTGTATGCAAGGATATGATAACAATAAATTAAC 3778
Db 3552 TTGCATGAACGAGTGATTAAATAAAAAATAAC 3582
RESULT 8
US-10-782-141-2
; Sequence 2, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
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; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2019)
US-10-782-141-2

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Query Match	12.5%	Score	747.2	DB 8	Length	2019;	
Best Local Similarity	69.8%	Pred. No.	2.5e-146;				
Matches 1143; Conservative	0;	Mismatches	423;	Indels	72;	Gaps	7;
QY	168	GTGAAAAGATGAGTCCATATCAAAATATAAAATCAATATGAAATATGGAAATCCTCATCG	227				
DB	1	GTGAAAATATGAATTCCTTATCAAAATACAAATGAATATGAAATCTCGAATGGTTCCTCCCG	60				
QY	228	AATAACACAATATGCGCAACACAGATATCCTTTTGGCAAAATATCGGATATGTCTACTATG	287				
DB	61	AATAACACAATATGTCACACAGATATCCTTTTGGCAAAAGNTCCAAATATATTTCTTAT	120				
QY	288	TCCTTGGAAATGTCAGGGAATCTCATGGATGAATTTGGGAATCAGTCGAAACGATA	347				
DB	121	AACTCGACGCTTTGTGAGGGAAGCCATGCAAGATACGTGGGAATCAGTCTCGGATATA	180				
QY	348	ACAAGTATTCGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAAT	407				
DB	181	GTAACCTATTCGGACATACCTTTATCAAAATCTTGCTAGAACCGGTATAGGTGGAATTCCT	240				
QY	408	ACACTATTAATCAATAATAGGAAACCTAAATCCGACTAATCGTCAAACTGTGTGACGACATT	467				
DB	241	GTAATATTTTCAATAATAAACAACCTATTCGGTCAAATCTGTGGCAGCACATT	300				
QY	468	TCTATATGATTTATTTATCTATTAATTCGTTAAAGAGGTAGCCGATAGTGTTTTAAGTGAT	527				
DB	301	TCTATATGATTTAGTATCTATTAATTCGTTAAAGAGGTAGACGAGACGCTGTTAAAGTGAC	360				
QY	528	GCGATTGCAGATTTGACGGTAAATTTGAAAATTTATAGAGAGTATATCTTTCTTATCTTT	587				
DB	361	GCGGTTGCAGATTTGAGGGTGAATGACTGCTTATCAAGATTATTAATCTCATTAATCTTT	420				
QY	588	GCGGCTTGGCTTTAAAGACGGTAAACCACTTTCAAAAGACAAATTAATCTGATATCGGACAA	647				
DB	421	GAGGATTGGCTTACAG-----ATAAATCAAACTCTAAAAAATTTGCTGAC	465				
QY	648	TTAGTTTATTTATTTTAAACCTTTCAGAAAGAGATTTCAATGCAAAATCTAGAGAGGTCAATTG	707				
DB	466	GTAGTTTAAACAGTTCCAAGCACGGGAAGAAGATTTCACTAAACCTTTTAGCAGGGTCATTA	525				
QY	708	TCAAGAAACAATGCTCAAGTATTTGTTATTAACCTACTTTTGCACAAGCTGCAAAATGTGCAG	767				
DB	526	TCAGACAGAAAGCTGNAATATTTATTTCCCTACGTTATGTGCAAGCTGCAATGTGCAAT	585				
QY	768	TTATTAATAATTAAGGATGCAAGTTCATATAAAGCACAATGGTTTCCCAATTTTGAAGTGCA	827				
DB	586	TTATTACTATTAAGGGACCGAGTTAAATAATAAAGAAAGATGGGACCTAGTGTGTCCACCG	645				
QY	828	GAGAATGTAAGATCGGNAATTAATATCACCTAAACAGTGGTGTGATTTTACCGGTGATTAC	887				
DB	646	TTGTATCCAGGGTTCAGGGAGAA-----CTGATGTG	675				
QY	888	TATGAGCGATTAATAATGCAAAACGGCAGAGTATACCAATATTTGTTTATATTCGTATCAG	947				
DB	676	AACGAGCGGTTAAAGCGGAAATAAAGAGTATACTAAATTTATTTGTGTAGGGTGGTATAC	735				
QY	948	GTAGGTTTAAATCAGATATAAACAGGGGGGACAGGTGCTGACACTTGGTTCGAAATTTAAT	1007				

Db	736	AAGGGTTTAGATCAGATAAGACAGCGCGGGTACAAGTCTGAAGTCTTGGTCCGAATTTTAAT	795
Qy	1008	AAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCACAACTTAT	1067
Db	796	AAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATGCTATATTTCCAACTTAT	855
Qy	1068	GAATTTTGAGAAATATCCATTTGCCAACACATGTTAGAGTTGACTAGGGAAATTTTATACAGAT	1127
Db	856	GAATTTTGAATAATATCCATTTAGCAACAAGTGTAGAGTTAACTAGGGAAATTTTATACAGAT	915
Qy	1128	GCAGTGGGATATTTCATCGGGAACTTATAGTTGGTTACGGAATTTGGCCCTAATACTTTTAAT	1187
Db	916	CCAGTGGGATATTTCAGGGGAAATATTAGTTGGGAACGGTTTT-----TTAGCTTTTAAT	969
Qy	1188	GGGTTAGAGGCTAATGGAACAGCGGGACCTGGTTTAGTTACTTTGGCTTAGCAAAATAGGT	1247
Db	970	TCGGTAGAAGCAATGGAACAGCGGGACCTGGTTTACTTTAGTTACTTTGGCTTACAGCTATAGAT	1029
Qy	1248	ATATATAATGAGTATGTT-----TCAGAGATATTTTCGCCGCTGGGTAGGNACTCGT	1298
Db	1030	ATATATAGTCAATCTATAATCTTACGTTGGTTATCTTAGTGGCTGGGGGGGAACCTCGT	1089
Qy	1299	CATTATGAAGACTACACAAAGGGTAAACGGTATTTTTCAACGCTATGTCCTGGAACCTACGAGT	1358
Db	1090	CATTATGAAGACTTCACAAAGGGTAAACGGTGTCTTTCAACGCTATGTCGGAACCTACGAGT	1149
Qy	1359	AATGATCTAGTAAATATGATTTTTTCAGAATGCCGATGTATATAAAATTACTTCAATTAGCT	1418
Db	1150	AATAATCCACGTAATATATTTTTTGGCAATACCGATATATTAAAAATTATTTTCATTAGCT	1209
Qy	1419	A--TCATGAACCTAGTAGGAGAGACTACCGCTAGACCAGAGTATCGTGTTCAAAGGCA	1475
Db	1210	AGATATGCATGCAACCGTTTGTGTGGGTATTTCAATCCACGGCATCTTGTTTTCAGTGTCA	1269
Qy	1476	GAATTTTCGTAGGGTAGGGGACCTGATTTTAAATTTATGATCAGGTAATAATGGCTAAGC	1535
Db	1270	GAATTTTTCGCAACACACTAAATACTTTCTCTGTATGAGGTAAACAGTCTCTGG---TAC	1326
Qy	1536	AGGATGACAATTTGAATCTACGTTCCCACTTGT-----ATTGCACCTAATGGTGTAGA	1589
Db	1327	TCACAGACAATTTGAATCTGTGTACCAAGGTATTATAAGGATCTACCACTAGTCGTGACA	1386
Qy	1590	GGACCTCTCATAGATTTATCAAAATGGCGCATGTGTGTATATGGAACCTCCAGAGTTAAC	1649
Db	1387	AAATTACTCTCATAGATTTATCAAAATGGCGCATGTGTTCAAAATGAACTCCAGAGTTAAC	1446
Qy	1650	GTATATGGTTGGACACATACAGTTTTTAAACGTGAAAAATATAATTGAGGCCAATCAAAATT	1709
Db	1447	GTATTTGGTTGSAACATACANGTATGAAAAAGATAATCGAAATTTTATCCAGATAAAATT	1506
Qy	1710	ACAAATAATCCGGCGGTGAAGAGTTATTACTTTCAAAATTTATCTGTCTATGCTATACC	1769
Db	1507	ACGCAATTTCTGCAGTAAAGCTTTTTCCTTACCAAGGATACAGGATATGCAGGAGT	1566
Qy	1770	TATGTAATAAAAGGCACT	1787
Db	1567	TAGTTCACAGCTGGGCT	1584

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RESULT 9
US-10-782-141-4
; Sequence 4, Application US/10782141
; Publication NO. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782.141

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; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
US-10-782-141-4

Query Match      12.4%; Score 739.8; DB 8; Length 2010;
Best Local Similarity 69.7%; Pred. No. 8.9e-145;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;

QY 177 ATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCGAATAACACA 236
Db 1 ATGAATTCCTTATCAAAATACAAATGAATATGAATTTCTGGATGGTTCCCGGAATAACACA 60

QY 237 AATACGCCAACACAGATATCCTTTTGCAATAAATCGGGATATGCTACTATGCTTCGGAAT 296
Db 61 AATATGTCAAACAGATATCCTTTTGCAAAAGGATCCAAATATATTTCTCTATTAACCTGGAC 120

QY 297 GATTTGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAAGTATT 356
Db 121 GCTTTGTCAGGGAAGGCCATGCGCAAGATACGTGGGAATCAGTCTCGGATATAGTAATTT 180

QY 357 GGGATAAATCTTATAGAGTTGTGATAGAACCTAGTTTGGGTGGGAATTAATACACTATTA 416
Db 181 GGGACATACCTTATACAAATTTCTTGCTAGAACCCGGTATAGGTGGAATTCCTGTAATATTT 240

QY 417 TCAATATAGGAAACCTAATTCGCACTTAATCGCTCAAACTGTGTCAGCACTTTCTATATGT 476
Db 241 TCAATATAAACAACTCATTCGCTCTTCTGGTCAATCTGTGGCAGACATTTCTATATGT 300

QY 477 GATTTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAAGTATGCGATTGCA 536
Db 301 GATTTAGTATCTATAATTCGTAAGAGGTAGACGAGAGCGGTGTTAAGTACGGGGTTGCA 360

QY 537 GATTTTGACGGTAAATGAAATTTATAGAGATATATCTTCTTTATCTTGGGGCTGG 596
Db 361 GATTTTGAGGGTGAATGACTGCTGTATCAAGATTTATATCTTCTTATCTTGGAGATTGG 420

QY 597 CTAAAGACGGTAAACCACTTCAAAAGACAAATAATTCGTATATCGGCAATTTAGTTTAT 656
Db 421 CTTACAG-----ATAATCAATCCTTAAAAAACCTTGTGACGTAGTTAAA 465

QY 657 TATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTAGGAGGGTCATTTGTCAGAAAC 716
Db 466 CAGTTCCAGACCGGGAAGAAGATTTCACTAAACTTTTAGCAGGGTCATTTATCAAGACAG 525

QY 717 AATGCTCAAGTATGTTATTAACCTACTTTTGCACAAGCTGCAAAATGTCAGTTTACTA 776
Db 526 AAGCTGAAATATTTATTTATGCTACGTATGTGCAAGCTGCAAAATGTCATTTTACTA 585

QY 777 TTAAGGATGTCAGTTCATATAAAGCACAATGTTCCCATTTTGTAGTCAGAGAATGTA 836
Db 586 TTAAGGACGCGAGTTAAATATAAAGAAATGGGACTAGTGTGTCACCGTTGTATCCA 645

QY 837 AGATCGGAATTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGA 896
Db 646 GGGTCAGGGAGAA-----CTGATTGTAACGAGCGG 675

QY 897 TTAATATGCAAAACGCGAGGATACCAATTAATTTTATATTTGGTATCAGGTAGGTTTA 956
Db 676 TTAAGGCGGAAAATAAAGAGAGTACTAATATTTGTAGGGGTGGTATAACAGGGGTTTA 735

QY 957 AATCAGATAAAACAGGGGGGACAGGTCGTGACACTTGGTCGAAATTTAATAAATTTTCTG 1016
Db 736 GATCAGATAAGACAGGGGGGTACAGTGTGTAAGTTTGGTCGAAATTTAATAAATTTCTG 795
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1017 AGAGAAATGACGCTTCGCGGTATTTGGATATATTCGCTATATTTCCAACTTATGATTTGAG 1076
796 AGAGAAATGACGCTTCGCGGTATTTGGATATATTTGCTATATTTCCAACTTATGATTTGAA 855
1077 AAATATCATTGCCAACACATGATAGAGTTGACTAGGGAATTTATACAGATCCAGTGGGA 1136
856 AAATATCATTAGCAACCAAGTGTAGAGTTAACTAGGGAATTTATACAGATCCAGTGGGA 915
1137 TATTCATCGGGAACTTATAGTTGGTTACGGAATTTGGCCTAACTATTTAAATGGGTTAGAG 1196
916 TATTCAGGGGAAATTTAGTTGGGAACGGTTTT-----TTAGCTTTAAATTCGGTAGAA 969
1197 GCTAATGGAACACGGGACCTGGTTAGTTACTTTGGCTTAGCAAAATAGGTATATATATAT 1256
970 GCAAAATGGAACACGGGACCTGGTTAGTTACTTTGGCTTCAAGCTATAGATATATATAGT 1029
1257 GAGTATGTT-----TCGAGATATTTTGGCGCTGGGTAGGAACCTCGTCAATTATGAA 1307
1030 CATTCTATTAATCTTCAGCTTTAGTTTATCTTAGTGGCTGGGGGGAACCTCGTCAATTATGAA 1089
1308 GACTACACAAAGGGTAAACGGTATTTTCAACGATATGCTCTGGAACTACGAGTAATGATCTA 1367
1090 GACTTCAACAAAGGGTAAACGGTCTTTTCAACGATATGCTCTGGAACTACGAGTAATGATCCA 1149
1368 CGTAATATTTGATTTTTCAGAAATCCGATATATATAAATTTACTTCAATTAGCTA---TCATG 1424
1150 CGTAATATTTTGGCAATACCGATATATTTTAAATTTATTTCAATTAGCTAGATATGCA 1209
1425 AACCTAGTAGGAGACACTACCGCTAGACGAGATATCGTGTTCAAAGGAGATTTTCGT 1484
1210 ATGCAACCGTTTGTGGGTATTTCAATCCACGGCATCTTGTTCACGTGCGAGAAATTTT 1269
1485 AGGGTAGGGGACCTGATTTAAATTTATGATGCAAGTAAATTAATGAGCTTAAGCAGGATGACA 1544
1270 CGGACAAACATTAATTAATTTCTGCTATGAGGTAAACAGTCTCTGGG---TACTCACAGACA 1326
1545 ATGGAATCTACGTTCCCACTTGT-----ATTGCACTCTAATGGTGTAGAGGACCTCT 1598
1327 ATGGAATCTGTTTACCAGGTATTAATGAGGATCTACCACTAGTCTGACAAATTAATCTCT 1386
1599 CATGATATTAATCAAGTCGCGCATGTTGTATATGGAACCTCAGAGTTAAACGTATATGCT 1658
1387 CATGATATTAATCAAGTCGCGCATGTTGTCAAAATGAAACCTCCAGAGTTAAACGTATTTGT 1446
1659 TGGACACATACAAAGTTTAAACGCTGAAATATAATTTGAAGCCAAATCAAAATTAACAAATA 1718
1447 TGGACACATACAAAGTATGAAATAAGATTAATCGAATTTATCCAGATATAAATTAACGAAAT 1506
1719 CCGCGGTGAAGAGTATTTACCTTCAAAATTTATCTTGTAAATGCTTATACCTATGTAATA 1778
1507 CCGTCAAGTAAAGCTTTTGCCCTACCAAGGATACAGGATATGTCAGGAGTTACGTCA 1566
1779 AAAGGCACT 1787
1567 GCTGGGCT 1575
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RESULT 10
US-10-120-544A-3
; Sequence 3, Application US/10120544A
; Publication NO. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
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FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4359
TYPE: DNA
ORGANISM: Bacillus popilliae
FEATURE:
NAME/KEY: CDS
LOCATION: (282)...(4229)
US-10-120-544A-3

Query Match 6.5%; Score 390; DB 5; Length 4359;
Best local Similarity 59.0%; Pred. No. 4.6e-71;
Matches 815; Conservative 0; Mismatches 535; Indels 54; Gaps 5;

QY 2292 AATAAGCGAAAGGTTGTGAGTCCCTATGTTTACAAGTAGTACGAAATAATACGTTAAAAA 2351
DB 2320 AAAAAGCAAGGAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAGGCGCTAAAG 2379
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCATTCTTATAGAAATGATGTCAGATG 2411
DB 2380 AAGCAGCAGCGATTATGAGATCGATCAAGCGGCAAGCGTGGTGGATTGATATCGGATG 2439
QY 2412 AACAAATCTCAGGAAAAAATAATGTTATGGATGAATAATGGAATGGAACCAACTTA 2471
DB 2440 ---AGTGTGACATGAGAAATGATCCTGTTAGTGAAGTAAATATGCAAAACAACTCA 2496
QY 2472 GTCAGTCTGTAATCTACTCAAAATGGACATTTTCT----- 2509
DB 2497 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTCGATGATCTATATCCAGCTCTGGAGA 2556
QY 2510 ---GGGAATGATGGACATTCGGTAATGATATATCATAGGATCCAATAATCCTATTTTTA 2567
DB 2557 GGGAGATCCATGGAAACAAAGTCCGCATGTTAGATCCGTCAAGATTAACCCGATTTTTA 2616
QY 2568 AAGGAAATTTCTACAGATCGGTGGAGCAGCAGACATATATGGAAC-----TCTATTTC 2621
DB 2617 AAGGCCATTATCTCAGTATGGCGGTGCGAAGCATATTGAGGCCACCAATGATACCTTCC 2676
QY 2622 CAACCTATATCTCTCAAAATAGATGAGTCTAAATTAATTAACCATATACAGTTATCGAG 2681
DB 2677 CCACGTATGCTATCAAAATATAGACGAAGCCCAATTAAGCCCATATACACGGTATAAAG 2736
QY 2682 TAAGAGGTTTGTGGGAAGTAGTAAAGATTGGAATTAATGTAACACGTTACGGGAAG 2741
DB 2737 TGGCGGGTTTGTGTAGCAGCAAGCTCTAGAGCTGTTGGTTACACGCTATAATGAAG 2796
QY 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTGGCCTATATGACGCCCTAACTTTCAT 2801
DB 2797 AAGTCGATGGATTTTAGATGTACCGGATAATATCCGCATGCGCGACTCTCTGTGCG 2856
QY 2802 GTGAGATTAATCGTGTGAATCATCGTC-----TCAGTATGTAGCGCAAG 2846
DB 2857 GTAAATTGATCATGCAAGCCCTATTTCGTATCCACCTTTTACAGATGTAAACCCCTG 2916
QY 2847 GGTATCTCACCAACAGATGGATATGCTCCCGATATGATGATGATGCCGCAAAATAG 2906
DB 2917 AGTTTAAATCAGATGCAACCATCTCTTGGCCACCAATCAGATGGTGCATTAATA 2976
QY 2907 ATAGAAGCATGTGAAGTGTACGATCGTCATCCATTTGATTTTCAATTTGACACCGGAG 2966
DB 2977 ACAGAAACACCCGAATGTATCAAGCGCATCAATTTGATTTCCATTTGATACCGGA 3036
QY 2967 AAGTAGATCAAAATACAAATGTAGTATGATGCTTTATTAATAATTTCTAATCCAGATG 3026
DB 3037 CAATCGATCTGGTGAAGATTGGGCAATTTGGGATGATCTTCAAAATCTGTGCCACAGATG 3096

QY 3027 GATACGCTACAGTAGGGAATCTAGAAGTCAATTGAAGAAGGACCACCTAAACAGGTGAAGCAT 3086
DB 3097 GTTACCGAAGCTTTAGATGATTTGGAAAGTGAATGAAGAAGAGCGCTGGGTGTGGAAGCAT 3156
QY 3087 TGGCAGATGTGAAACAAAAGGAAAGAAATGGAACAACAACATGGAAGAAAAACGTTGGG 3146
DB 3157 TAGAACTTGTCAAGAAAGAGAAAGAAATGGAGACATCAGAAGGAGCAGCAGCTGTTCCG 3216
QY 3147 AAACACAACAGCCTATGATCCAGCAAAACAGCCTGTAGATGCAATTTATTACAAA----- 3201
DB 3217 AAACGAACAACAATATGATGCGGCCCAACACGCGGTGATGGCGTTTATTTCACAAACACGC 3276
QY 3202 -TGAACAAGAGTTACACTATATATTACTTTAGATCATATTTCAAAACGCTGATCGACTGG 3260
DB 3277 GCTATGAAAATTTGAAGTTGGAACAACCATCTCCCAATATTTGTATGCTGATCATCTCG 3336
QY 3261 TACAGTCGATTCCTATGATATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACATG 3320
DB 3337 TGCAGTCGATTCCTTATGATATAATAATAATATGTAACCGGAAGTTCCAGGTATGAATTAACG 3396
QY 3321 ATGTATATCAAGGTTAAACGCAAGCTATCATGCAAGGTTATTAATTTATATGATGCAAGAA 3380
DB 3397 AACTCTATACAGAGCTAAACACTCTCGTTTCAAGATCGTTCTATCTATATGACACGCGGA 3456
QY 3381 ATGTCTATAACAATGCTGACTTTTACACAAGGATTACAGGATGCGCAACAGGAAATG 3440
DB 3457 ATCTGATTAATAATGGCGCTTTAGCAATGGGCTTATGATTGGCAGGCTACCCCGCATG 3516
QY 3441 CCGCGGTACAACAATAATGAGTGGAGCTTCAGTATTTAGTTCTTATCAAAATGGAGCGCGGGG 3500
DB 3517 CACGAGTGGAAACAAGAAATATGAGAAATCTGTACTGCTGCCAAATGGGATGCCAATG 3576
QY 3501 TATCTCAAACTTGCATGCTCAAGATCATCATGATATGTTACGTGATTTGCCAAA 3560
DB 3577 TGTGCGAAGATCTTTGTATGCAACAATCGCGGTTATGATTTGCGTGTACGCGCGAGAA 3636
QY 3561 AAGAGGACCTCGMAAAGGTTATGTAACGATGATGATGTAATGGAAGAGCAGGAAACAC 3620
DB 3637 AAGAGATCGGAGCTGGCAATGTTACCTTCAGTACTGTGCAAAACCATGTGCAACAGC 3696
QY 3621 TTAAGTTCACTTTTCGCAAGAG 3644
DB 3697 TGAGCTTTACTTCTTGGCATATAG 3720

RESULT 11
US-11-091-654-3
Sequence 3, Application US/11091654
Publication No. US20050172355A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriochi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,654
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4359
TYPE: DNA

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; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-654-3

Query Match          6.5%; Score 390; DB 10; Length 4359;
Best Local Similarity 59.0%; Pred. No. 4.6e-71;
Matches 815; Conservative 0; Mismatches 535; Indels 54; Gaps 5;

Qy 2292 AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTAGCGAAAAATACGTTAAAAA 2351
Db 2320 AAAAAGCAAGGAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAAAGCGCTAAAG 2379

Qy 2352 TAGAAACGACAGATATTGAAATAGATCAAGGGCCATTTCTATAGAAATGATGTCAGATG 2411
Db 2380 AAGCAGCGCCGATTTATGAGATCGATCAAGCCGCAACGTTGGTGGATTGTATATCGGATG 2439

Qy 2412 AACAAAAATCCTCAGAAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTA 2471
Db 2440 ---AGTGTGCNATGAGAAATGATCCTGTTAGATGAATTAATATGCAAAACAACCTCA 2496

Qy 2472 GTCAGTCTCGTAATCTACTCCAAATGGAGACTTTTCT- 2509
Db 2497 GCCAAGCCCGCAATTACTGCTCAATGGGAATTTCCGATGATCTATATCCAGCTCTGGAGA 2556

Qy 2510 --GGGAATGATTGGACATTCGGTAAATCATATTATCATAGGATCCATAAATCCTATTTTTA 2567
Db 2557 GGGAGAATCCATGGAANAACAAAGTCGGCATGTTACGATCCGTCGAAGATAACCCGATTTTTA 2616

Qy 2568 AAGAAAAATTTCTACAGATCGTGGAGCAGAGACATATATGGAAC-----TCTATTTC 2621
Db 2617 AAGGCCATTATCTCAGTATGCGGTTGCGAACGATATTAGGCCACCATAATGATACCTTCC 2676

Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAACCATATACACGTTATCGAG 2681
Db 2677 CCAGTATGCTATCAAAAAATAGACAAGACGCAAAATTTAAAGCCCATATACACGTTATAAG 2736

Qy 2682 TAAGAGGTTTGTGGGAAGTAGTAAAGATTTGAAATTTAATGGTTAACACGTTACGGGAAG 2741
Db 2737 TGC CGGGTTTGTGGTAGCAGCAAGACTCTAGAGCTGTGGTTACAGGCTAATATGAAG 2796

Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGACGCCTAAATCCTTCAT 2801
Db 2797 AAGTCGATGCGAATTTTAGATGTACCGGATAATATCCGCGATGCGCCGACTCCTGTCTGCG 2856

Qy 2802 GTGGAGATTATCGGTGTGAATCATCGTC-----TCAGTATGTGAGCCAAAG 2846
Db 2857 GTGAATTTGATCGATGCAAGCCCTATTTCGTATCCACCTTTACTTCCAGAAATGTAACCCCTG 2916

Qy 2847 GGATCTCTACCAACAGATGGATATGCTCCCGATATGTATGTCATGCCCAAAATATAG 2906
Db 2917 AGTTTATAAATCAGATGCAACCATCTCTTGGCCACCACAATCAGATGGTCGATTACAATA 2976

Qy 2907 ATAGAAAGCATGTGAAGTGTACAGATCGTCAATTCATTTGATTTTTCATATTGACACCGGAG 2966
Db 2977 ACAGAAACACCCGAAATGTCAATCAAGCGCATCAATTTGATTTGATTTGATATACCCGGGA 3036

Qy 2967 AAGTAGATACAAATACAAATGTAGTATGTATGTCCTTATTAAAAATTTCTAAATCCAGATG 3026
Db 3037 CAATCGATCTGGTCGAAGATTTGGGCATTTGGGTGATCTTCAAAATCTGTGCCACAGATG 3096

Qy 3027 GATACGCTACAGTAGGGAATCTAGAAGTCAATTGAAAGAGAGGCCACTAACAGGTGAAGCAT 3086
Db 3097 GTTACGCAAGCTTAGATGATTTGGAAGTGAATTTGAAGAGAGGAGCGCTGGGTGTGCGAAGCAT 3156

Qy 3087 TGGCACATGTGAACAAAGGAAAGAAATGGAACCAACATCGAGCAAAAAAAGCTTTGGG 3146
Db 3157 TAGAATTTGTCAAGAAAGAGAAAGAAATGAGACATCAGAGGACGACGACTGTTTCG 3216

Qy 3147 AAAACAACAAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTTATACAAA----- 3201
Db 3217 AAAAGAAACAAAATATGATCGGCCCAAAACACGGGGTGTAGTGGCGTTATTCACAAAACACGC 3276

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Qy	2341	TACGTTAAATAATAGAAACGACAGATATATGAAATAGATCAAGCGGCCATTTCTATAGAAATG	2400
Db	2073	TGCCTTACAGACAAGTAGTGTAAACGGATATTAAGTGAATCAAGCGGCAAACTTAGTAGAATG	2132
Qy	2401	TATGTCAGATCAAAACAAATCCTCAGGAAAAATAATGTTATGGCATGAAATAAACCTGGC	2460
Db	2133	CCTATCCGATGAGTTATACCCAAATGAAAACGAAATGTTATGGGATGCAGTGAAGAGGC	2192
Qy	2461	AAAAACAATTAGTCAGTCTCGTAATCTACTCCAAAAATGGAGACTTTTTCTCGGAATGAT--	2518
Db	2193	GAACGACTTGTTCAGGCACGTAACCTTACTCCAAGATACAGGCTTTAATAGGATTAATCG	2352
Qy	2519	-----TGGACATTCGGTAATGATATATCATAGGATCCAAATATCTCTATTTTTAA	2568
Db	2253	AGAAAAACGGATGGGACGGGAATCGGGAAATCGAGGTTTCGGGAAGGAGATGTTCTGTTTAA	2312
Qy	2569	AGGAAAAATTTCTACAGATGCGTGAGCAGACAGACATATATGGAATCTTATTTCCAACTTA	2628
Db	2313	AGATCGTTCGCTTCGTTTGACAAGTCGAGAGAGATTTGATACGAAACATATCCACGTA	2372
Qy	2629	TATCTGTCAAAAAATAGATGAGTCTAAATTAATAAACCATATATACAGTTTATCGAGTAAGAGG	2688
Db	2373	TCTCTATCAACAAATAGATGAATCACTTTTAAAAACCATATACAGATATATAACTAAAGG	2432
Qy	2689	GTTTGTGGGAAGTAGTAAGAATTTGAAATTTAATCGTTAAACGTTACGGGAAAGAAATTTGA	2748
Db	2433	TTTTATAGGAAGTAGTCAAGATTTTAGAGATTTAAATTAATACGTATCATCGGCAAAATCAAT	2492
Qy	2749	TGCTATCATGAATGTTCCAAATGATTTGGCTATATGCAGCCATAATCTTTTCATGTGGAGA	2808
Db	2493	CGTCAAAAATGTACCAAGATATCTTTGCCAGATGTATCTCCCTGTCAAAATTTCTTTGGTGG	2552
Qy	2809	TTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTTACACCAACAGATGG	2868
Db	2553	GATCGATCGCTGCAGTCAGTCAGCAACAGTATGTAGACGGCAATTTAGCTCTCGAAACATATG	2612
Qy	2869	ATATGCTCCCGATATGTATGATGATGCCCGCAAAAATATAGATAGAAAGCATGTGAAGTGTCA	2928
Db	2613	AGAAAATGGAAAATATGTCCTCT-----2634	
Qy	2929	CGATCGTCATCCATTTTCATTTTCATATTGACCGGAGAAGTAGATACAAATACAAATGT	2988
Db	2635	-GATTCCTCATGCTTTCTTTCCATATGTGATACAGGTGAAATAGATTTGAATGAAATATC	2693
Qy	2989	AGGTATTTGATGTCCTTATTAATAAAATTTCTAATCCAGATGGATAGCTTACAGTCGGGAATCT	3048
Db	2694	AGGAAATTTGGTCGTATTTAAATTCGACAACAATGGATAGCGAACACTAGGAATCT	2753
Qy	3049	AGAAGTCATTTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCCATGTGTGAACAAAGGA	3108
Db	2754	TGAATTCGTAGAAAGAGGGCCATTTGTCAAGGGGAAACATTTAGAACGAGCAACAAACAAGA	2813
Qy	3109	AAAGAAATGAAAACAACACATGGAGAAAAAACGTTGGGAAACAACAAGACCTTATGATCC	3168
Db	2814	ACAAATGTGAAGACAAAAATGGCAAAAAACGTGGGGCATCAGAAAAGCATATTATGTC	2873
Qy	3169	AGCAAAACAGGCTGTAGATGCATTTATTAACAATGAAACAAGAGTTACACTATCATATTAC	3228
Db	2874	AGCAACCAAGCCATTGATCGTTTATTCGCAGATATATCAAGACAAAAAATTTAATTTCTGG	2933
Qy	3229	TTTAGA-----TCATATCAAAACGCTGATCGCATGGTACAGTCGATTTCCCTTATGTATA	3282
Db	2934	TGTAGAAATGTCAGATATGTTGGCAGCCAAAACCTTGTACAGTCCATTCTCTTACGTATA	2993
Qy	3283	CCATAATTTGGTTACCGAATGCTCCAGGTATGAACCTATGATGTATATCAAGAGTTAAACGC	3342
Db	2994	TAATGATGCGGTTACCGAAAAATCCCTGGAAATGAACTATACGAGTTTACAGAGTTAACAA	3053
Qy	3343	ACGTATCATCGAAGGTTATAATTTATATGATGACCGAAATGTCTATACAAAATGGTCACATT	3402
Db	3054	TAGACTCAACACAGCATGGAATTTGTATGATCTTCGAAATGTCTATACCAATGGAGATTT	3113
Qy	3403	TACAAGGATTACAGGGATGGCACGCAACAGGAAATGCGCGGTATCAACAAATGATGATG	3462

RESULT 13

US-10-089-678-3

; Sequence 3, Application US/10089678

; Publication No. US20030017967A1

GENERAL INFORMATION:

APPLICANT: ASANO, Shinichiro

; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,

; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

; FILE REFERENCE: Q68821

; CURRENT APPLICATION NUMBER: US/10/089,678

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: JP 2000-236140

;
; PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: PCT/JP01/06660

PRIORITY FILING DATE: 2001-08-02

: NUMBER OF SEO ID NOS: 3

: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: Patent In version 3.1

: SEQ ID NO 3

: LENGTH: 3690

LENGTH: 30
TYPE: DNA

; LIFE: DNA
; ORGANTSM: Bacillus thuringiensis

US-10-089-678-3

Query Match

Query Match 6.4%; SCORE 380.8; DB 3
Best Local Similarity 55.4%; Pred. No. 3 7e-69.

Best local similarity 33.4%; Fied. NO. 3.7e-65;
Matches 881: Conservative 0; Mismatches 622; Indels 87; Gaps 1.

Qy	2221	ACGGGTGAACGATCTGTTTACCAATTTAAACAAAAATAATTTACTAGAAATAGGTGGTATT	2280
Db	2139	AGGAGGAGAAGTTTATGTGTAGATTAAGTTCGAACCTTATTCGGTAAATGCAACATTTTGAAGC	2198
Qy	2281	GCTGTTTAACAAAATAAGCGAAAAAGGTGTGGAGTCCTATGTTTACAAGTAGTAGCAAAAA	2340
Db	2199	AGAAGAAGACCTAGATGTGGCAAGAAGACAGTAAATGGCTGTTTACGAGTAAAAAAGA	2258
Qy	2341	TAGCTTTAAATAGAAACGACAGATTTAGAAATAGATCAAGCGGCCATTTCTATAGAATG	2400
Db	2259	TGCTTTACAGACAAGTGTAAACGGATTATCAAGTGAATCAAGCGGCAAACTTAGTAGAATG	2318
Qy	2401	TATGTCAGATGAACAAAATCCTCAGAAAAATAATATGTTATTGGATGAAATAAAACTGGC	2460
Db	2319	CCTATCCGATGAGTTATACCCAAATGAAAAACGAATGTTATTGGGATGCAGTGAAGAGGC	2378
Qy	2461	AAAAACAACCTTAGTTCAGTCTCGTAAATCTACTCCAAAATGGAGACTTTTCTGGGAATGAT--	2518

Db 2379 GAAACGACTTGTTCAGGACGTAACCTTACTCCAGAGATACAGGCTTTAATAGGATTAATCG 2438
Qy 2519 -----TGACACATTCGGTAATGATATATATCATAGATCCAAATAATCCTATTTTAA 2568
Db 2439 AGAAAAACGATGCGAGGGAATACGGGAATCGAGGATTCGGAAGGAGATGTTCTGTTAA 2498
Qy 2569 AGGAAATTTCTACAGATCGGTGGACACAGACATATATGNACTCTATTTCCAACTTA 2628
Db 2499 AGATCGTTCGCTTCGTTGACAAAGTCGAGAGGATTTGATACAGAAACATATCCAACTGA 2558
Qy 2629 TATCTCTCAAAAATAGATGAGTCTAAATTAATAACCATATACACGTTATTCGAGTAAGAG 2688
Db 2559 TCTCTATCAACAATAGATGATCACTTTTAAACCATATACAGATATTAACATAAGG 2618
Qy 2689 GTTGTGGGAAGTAGTAAGATTTGAAATTTAATGGTAAACAGTTACGGGAAAGAAATGGA 2748
Db 2619 TTTTATAGGAAGTAGTCAAGATTTAGAGATTTAAATTAATACGTCATCGGGCAATCAAT 2678
Qy 2749 TGCTATCATGAATGTTCCAAATGATTTGGCTATATGCAAGCTTAATCCTTCATGTGGA 2808
Db 2679 CGTCAAAAATGTACAGATAATCTCTGGCAGATGTACTCCCTGTCAATTTCTTGTGGTG 2738
Qy 2809 TTATCGCTCTGAATCATCTCTCAGTATGTGAGCCAAAGGTATCTTACACCAACATCGG 2868
Db 2739 GATCGATCGCTGAGTACGACAGTATGTAGACGGAATTTAGCACTCGAAACAAATGG 2798
Qy 2869 ATATGCTCCCGATATGATGTCATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCA 2928
Db 2799 AGAAATGCAAAATATGCTCTCT ----- 2820
Qy 2929 CGATCGTCTCAATTTGATTTTTCATATTTGACACCGGAGATAGATACAAATACAATGT 2988
Db 2821 -GATTCCTTCCATGCTTTCTTCCATATGATACAGGTGAATAGATTTGAATGAAATATAC 2879
Qy 2989 AGTATTTGATGTCTTATTAATAATTTCTAATCAGATGGATAGCTACAGTGGGAATCT 3048
Db 2880 AGGAATTTGGTTCGATTTTAAATTCGACACAAATGATAGCAGCACTAGGAATCT 2939
Qy 3049 AGAAGTCATTTGAAGAGGACCACTAAACAGTGAAGCATTTGGCACTGTGAAACAAAGGA 3108
Db 2940 TGAATTTGGTAGAAGAGGGCCATTTGTGAGGGAAACATTTAGAACGAGCAACAAACAGA 2999
Qy 3109 AAAGAAATGGAAACACATGAGAGAAACCTTGGGAAACACACACAGCCCTATCATCC 3168
Db 3000 ACAACATGGCAAGACAAATGGCAAGAAACGTTGGGCGATCAGAAAAAGCATATTATGC 3059
Qy 3169 AGCAAAACAGGCTGTAGATGCTATTTTACAAATGAACAGGTTACATCATATTTAC 3228
Db 3060 AGCAAGCAAGCATTTGATCGTTTATTCGAGATTTATCAAGACCAAAACTTAATTTCTGG 3119
Qy 3229 TTTAGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCCGATCCCTPATGTATA 3282
Db 3120 TGTAGAAATGTCAGATATGTTGGCAGCCCAAAACCTTTGACAGTCCATTCCTTACGTATA 3179
Qy 3283 CCATATTTGGTTACCGAATGCTCCAGTATGACTATGATGATATATCAAGAGTTAAACGC 3342
Db 3180 TAATGATGCTTACCAAGAAATCCCTGGAATGAATATACGAGTTTACAGAGTTACAAA 3239
Qy 3343 AGGTATTCATGCAAGGTTTAAATTTATATGATGACGAAATGTCTAACAAATGGTGACTT 3402
Db 3240 TAGACTCCAACAGCATGGAATTTGATGATCTTCGAAATGCTATACCAATGGAGATTT 3299
Qy 3403 TACAAAGGATTTACAGGATGGCAACAGAGAAATGGCGGTTACAACTTCAACAAATGGATGG 3462
Db 3300 TCGAAATGGAATTAAGTGAATGGAAATGCAACATCAGATGGAATGTGCAACAACTAAGCGA 3359
Qy 3463 AGCTTCAGTATGATTTCTATCAATTTGGAGCGGGGGTATCTCAAACTTGCATCTCA 3522
Db 3360 TACATCTGCTTGTCAATTCCAAACCTGGAATTTCAAGTGTCAACAAATTTACAGTTCA 3419
Qy 3523 AGATCATATGGATATGTGTGTAGTGTGTTGTCAAAAAGAGAGGACCTGGAAAAAGGGTA 3582
Db 3420 ACCGAATTATAGATATGTGTACGTGTCTACAGCGAGAAAGAGGAGTAGGACCGGATA 3479

Qy 3583 TGTATACGATGATGGATTTGTAATGGAAAGCAGAGAAACACTTAAGTTCACTTCTTGGCAAGA 3642
Db 3480 TGTGATCATCCGTGATGGTGCGAATCAGACAGAAACACTCAATTTAATATATGTGATGA 3539
Qy 3643 AG-----GATATATGACAAACACAGTAGAGGTATT 3672
Db 3540 TGATACAGGTGTTTTATCTGCTGATCAAACTAGCTATATACAAAAACAGTGGAAATCAC 3599
Qy 3673 CCCGAAAGTGCATCGTGTACCGGATTTGAAATAGGAGAAACCGAAGGTACATTTTATATAGA 3732
Db 3600 TCCATCTACAGACGAAGTTTGGATTGACATGATGAGACCGAAGGTGATTATCAACATAGA 3659
Qy 3733 TAGCATCCGAGTTGCTTTGTATGCAAGGATA 3762
Db 3660 AAGTGTAGAACTCGTGTTAGAAGAAGATA 3689

RESULT 14

US-10-120-544A-19
; Sequence 19, Application US/10120544A
; Publication No. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Maeo
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/10/120,544A
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-10-120-544A-19

Query Match 5.3%; Score 318.6; DB 5; Length 4366;
Best Local Similarity 55.7%; Pred. No. 4.8e-56;
Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;
Qy 2292 AATAAGCGAAAAAGTTGTGAGTCTCTATGTTTACAGTAGTAGCAAAAAATACGTTAAAAA 2351
Db 2196 AAAAAAGCAAGGAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAAAGCGGCTAAAAAG 2255
Qy 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAACTGTATGTCAGATG 2411
Db 2256 AAGACACGACCGATTATGAGATTGATCAAGCGCCCAACGCTGGTAGTGTATATCGGATG 2315
Qy 2412 AAAAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAAACCTGGCAAAACAACTTA 2471
Db 2316 ---AGTGTGACATGATAAAATGATCCTCTGTAGATGAAGTAAAAATATGCAAAACAACTCA 2372
Qy 2472 GTGAGTCTGTAATCTACTCCAAAATGGAGACTTTTCT----- 2509
Db 2373 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTTTCGATGATCTATATTCAGCTCTCGAGA 2432
Qy 2510 ---GGGAATGATTGGACATTCGGTAAATGATATTATCATAGGATCCAAATAATCCTATTTTAA 2567

Db 2433 AGGAGAAATCCATGGAAACCAAGTCCGAATGTTACGATCCGACAGATAAACCCGATTTTGA 2492
Qy AAGGAAATTTCTACAGATCGTGGAGCAGAGACATATATGGAC-----TCTATTTC 2621
Db 2493 AAGCCATTAATCTCAGTATGGCGGTGCGAACGATATCGAGGCCACCAATGATACCTTCC 2552
Qy 2622 CAACCTATATCTGTCAAAAATAGATGAGTCTAAATTTAAACCATATACACGTTTATCGAG 2681
Db 2553 CCAGTATGCTATCAAAAAATAGACGAAGCCAAATTTAAAGCCGTATACACGTTATTAAG 2612
Qy 2682 TAAGAGGGTTGTGGAGAGTAGTAAGATTGAATTTGAATTTGAATGTTAAGCAGTTACGGGAAAG 2741
Db 2613 TGGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTTGGTTACACGCTATAATGAAG 2672
Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTGGCCTATATGCGACCTTAATCCCTTCAT 2801
Db 2673 AAGTTGATGCTATTTAGATGTTACCGGATTAATATCCCGCATGCGCCGACTCTGTCTGCG 2732
Qy 2802 GTGGAGATTATCGTGTGAATCATCGTCTCAGT-----ATGCTCCCG 2879
Db 2733 GTGAATTTGATCGATGCAAGCCCTATTTCGTATCCACCTTTACTTCCAGATGTAACCCCTG 2792
Qy 2835 -----ATGTGAGCCAGGGTATCTTACACCAACAGATGGAT----- 2870
Db 2793 AGTTTAAATCAGATGCAACCATCTCTTGGCACCACCAATCAGATGGTTCGATTACAATA 2852
Qy 2871 -----ATGCTCCCG 2879
Db 2853 ACATGAACAGCAGCAGGATGTAACATGTAATCCTTAGCATGAATCTCCCTTACGCGCTG 2912
Qy 2880 ATATGATGATGCCCGCAAAATATAGATAGAAGCATGTGAAGTGTACAGATCGTCATC 2939
Db 2913 AAATAGCATCCAGCAAGTGGATTCCGCGAGAAACATCGCAATGTCTCAAGCGCATC 2972
Qy 2940 CATTTGATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGATAGGTATTGATG 2999
Db 2973 AATTTGAGTTCCACATTTGATGATACCGGACATCGATTTTGTGCGAAGATTTGGCGATTTGGG 3032
Qy 3000 TCTTTTAAAAATTTCTAATCCAGATGGATACCTACAGTACAGTACAGTACAGTACAGTACAGT 3059
Db 3033 TGATCTTCAAAATCTGTGCCAGATGGATGATACCAAGCTTAGATGATCTGGAAGTGAATG 3092
Qy 3060 AAGAAGGACCACTAACAGGTGAAGCATTTGGCAGATGTGAACAAAAAGGAAAGAAATGGA 3119
Db 3093 AAGAAGGAGCGTGGTGTGCGAAGCATTAAGACTTGTCAAAAAAGGAAAGAAATGGA 3152
Qy 3120 AACACACATGGAGAAAAAAGTGGGAAACACAAAGCCTATGATCCAGCAAAACAGG 3179
Db 3153 GACATCAGAGGAGCAGCACTGTTCGCAACGAAACACAAATATGATGCGGCCCAACATG 3212
Qy 3180 CTGTAGATGCATTTTACAAATGAAC-----AAGAGTTACACTATCATATTACTTTAG 3233
Db 3213 CGGTGATGGGTTTATTACAAACAGCGGTATGAAAATTTGAAGTTTGAACCAACCATTT 3272
Qy 3234 ATCATATTCAAAACGCTGATCGACTGGTACAGTTCGATTCCTATGTATACCAATAATGGT 3293
Db 3273 CTGACATTTGTATGCTGATCATCTCGTGCAGTCTGATTCCTTATGATATATTAATATG 3332
Qy 3294 TACCGAATGCTCAGGTATGAATCTATGATGATATCAAGAGTTTAAACGCAAGTATCATGC 3353
Db 3333 TACCGAAGTTCCAGGTATGAATTTAGCAACTCTATTTCAGAGCTTAAACACACTGGTTTACA 3392
Qy 3354 AAGGTTATATTTATGATGACGAAATGTCTATACAAATGTGTGATCTTACACAGGAT 3413
Db 3393 ATCGGTTCTACCTGTATGACCGGAAATCTGAATTAATAATGGCGCTTTAGCAATGGGC 3452
Qy 3414 TACAGGGATGGCAGCAACAGGAAATGCCCGGTACAAACAAATGGATGGAGTTCAGTAT 3473
Db 3453 TTATGATTTGGCAAGCTACTCTCATGCAAGATGAGCAAGATATGAAATCGGTGC 3512
Qy 3474 TAGTTCTATCAAAATGGAGCGGGGTATCTCAAAATTTGCAATGCTCAAGATCATCATG 3533
Db 3513 TCGTGTGCAAAATTTGGGATGCCAATGTGTGCGAAGATCTTTGTATCGAACAACAAATCGCG 3572

Qy 3534 GATATGTTTACGTTGATTTGCCAAAAAGAGGACCTCGAAAAAGGATATGTAAACGATGA 3593
Db 3573 GTTATGTTTTCGCTGTACGCGGAGAAAGATCCGGAGCTGCGCAATGTTTACCTTTA 3632
Qy 3594 TGATTTGTAATGAAAGCAGGAAACACTTAAAGTTTCACTTCTTCGGAAGAG 3644
Db 3633 GTGACTGTGAAATCATGTGCAAGCTGAGCTTTACTTCTTGGATATAG 3683

RESULT 15

US-11-091-654-19
; Sequence 19, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; FILE REFERENCE: Op1335
; CURRENT APPLICATION NUMBER: US/11/091,654
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-654-19

Query Match 5.3%; Score 318.6; DB 10; Length 4366;
Best Local Similarity 55.7%; Pred. No. 4.8e-56;
Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;
Qy 2292 AATAAGCGAAAAAGGTTGTGAGTCTCTTACAAAGTAGTACGAAAAATACGTTAAAAA 2351
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Qy 2352 TGAAGACGACAGATTATGAAATAGATCAAGCGGCCATTTCATAGAAATGTATGTCTAGATG 2411
Db 2256 AAGACACGACCGATTATGATGATTGATCAAGCGCCCAACGTTGATATATCGATG 2315
Qy 2412 AACAAAATCCTCAGGAAAAATATCTTATGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2316 ---AGTGTGGACATGATAAAATGATCCTGTTAGATGAAGTAAATATGCAAAACAACTCA 2372
Qy 2472 GTCAAGTCTCGTAACTTACTTCCAAAAATGGAGACTTTTCT----- 2509
Db 2373 GCCAGCCCGCAATTTACTGCTCAATGGAAATTCGATATCTATATTCAAGTCTCGAGA 2432
Qy 2510 ---GGGAATGATTGGACATTCGGTAAATGATATATTATCATAGATCCAAATATCTTATTTTA 2567
Db 2433 AGGAGAAATCCATGGAAAAACAAAGTCGAAATGTTACGATCCGACAAAGATAACCCGATTTTA 2492
Qy 2568 AAGGAAAAATTTCTACAGATGCGTGGAGCAGGACAGATATATGGAAC-----TCTATTTC 2621
Db 2493 AAGGCCATTTATCTCAGTATGGCGGGTGGCAACGATATCGAGGCCACCAATGATACCTTCC 2552
Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTTAAATTTAAAAACCATATACACGTTATCGAG 2681

Db 2553 CCACGTATGTCGTATCAAAAATAGACGAAGCCAAATTAAGCCGTATACACGTTATAAAG 2612
Qy 2682 TAAGAGGGTTGTGGGAAGTAGTAAAGATTGAAATTAATGGTAAACACGTTACGGGAAAG 2741
Db 2613 TGGCGGGTTGTGGCAGCAGCAAGCTCTAGAGCTGTGGTTACACGCTATATGAAG 2672
Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTCAT 2801
Db 2673 AAGTTGATCGATTTTAGATGTACCGGATAATATCCGCATGCGCGACTCCTGTCGCG 2732
Qy 2802 GTGGAGATTATCGCTGATCATCGTCTCAGT-----ATGCTCCCG 2879
Db 2733 GTGAATTTGATCGATCGAAGCCCTATTTCGTATCCACCTTTACTCCAGAAATGTAAACCCTG 2792
Qy 2835 -----ATGTGAGCCAGGGTATCCTACCAACACAGATGGAT----- 2870
Db 2793 AGTTTATAAATCAGATGCAACCATCCTCTTGGCCACCACCAATCAGATGGTCGATTACAATA 2852
Qy 2871 -----ATGCTCCCG 2879
Db 2853 ACATGAACACGACGACGAGTACTACCATGAATCCTAGCATGAATCCTCCCTTACGCCCTG 2912
Qy 2880 ATATGTAATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACGATCGTCAATC 2939
Db 2913 AAATAGCATCCAGCCAAAGTGGAATCGGCAGAAAACATCGCAAAATGTCTCAAGCGCATC 2972
Qy 2940 CATTTGATTTTCATATTGACCCGGAGAGTAGATACAAATACAAATGTAGGTATTGTG 2999
Db 2973 AATTTGAGTTCCACATTTGATACCGGGACAATCGATTTGGTCGAAGATTTGGGCAATTTGGG 3032
Qy 3000 TCTTATTAATAATTTCTAATCCAGATGGATA CGCTACAGTAGGGAATCTAGAAATCAATTG 3059
Db 3033 TGATCTTCAAAATCTGTGCCACAGATGGATACGCAAGCTTAGATGATCTGGAAGTGATTG 3092
Qy 3060 AAGAAGGACCTAAACAGGTGAAGCATTGCACATGTGAACAAAGAAAGAAATGGA 3119
Db 3093 AAGAAGGAGCGTTGGGTGCGAAGCAATTAAGACTTGTCAAAAAGAGAAAGAAATGGA 3152
Qy 3120 AACAAACATGGAAGAAAAAGCTTGGGAAACACAAAGCCTATGATCCAGCAAAACAGG 3179
Db 3153 GACATCAGAAGGAGCAGCACTGTTCCAAACGAAACACAAATATGATCGGCCCAACATG 3212
Qy 3180 CTGTAGATGCATTTTACAATGAAC-----AAGAGTTACACTATCATATTACTTTAG 3233
Db 3213 CGGTGATGCGGTTATTACAAACAGCGCTATGAAAAATTGAAGTTTCGAAACAAACCATTT 3272
Qy 3234 ATCATATTCAAACGCTGATCGACTGTCAGTGCATTCCTATGATATACCATTAATTGGT 3293
Db 3273 CTGACATTTTGTATGCTGATCATCTCGTGAGTCGATTCCTTATGATATATAAATATG 3332
Qy 3294 TACCGAATGCTCCAGGTATGAATCATGATGATATCAAGAGTTTAAACGCACGTCATCATGC 3353
Db 3333 TACCGGAAGTCCAGGTATGAATTAACGAATCTATTACAGAGCTAAACACACTGGTTTCAGA 3392
Qy 3354 AAGGTTATATTTATATGATGCAGAAATGTCTATAACAAATGGTGAATTTTACACAGGAT 3413
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Db 3453 TTATGCATTTGGCAAGCTACTCTCATGCAAGATAGACAGAAATAGAAATCGGTGC 3512
Qy 3474 TAGTTCTATCAATTCGAGCGGGGGTATCTCAAAATTCATGCTCAAGATCATCATG 3533
Db 3513 TCGTGTGCCAAATTTGGGATGCCAATGTGTGCAAGATCTTTGTATCGAAACAAATCGCG 3572
Qy 3534 GATATGTTTACGTGTGATTTGCCAAAAGAGGACCTGGAAAAGGGTATGTAAAGATGA 3593
Db 3573 GTTATGATTTGGGTGTGTCAGGCGAGAAAAGAGATCCGGAGCTGGCAATGTTTACCTTTA 3632
Qy 3594 TGGATTGTAATGGAAAGCAGGAAACACTTAAGTTTCACTTCTTTCGGAAGAG 3644
Db 3633 GTGACTGTGAAATCATGTCCGAAGCTGAGCTTTACTTCTTTCGGATATAG 3683

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 14:38:00 ; Search time 390.161 Seconds
(without alignments)
7512.972 Million cell updates/sec

Title: US-10-781-979-1

Perfect score: 5980

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New.*
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10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	6.5	4359	9	US-11-091-643-3
2	318.6	5.3	4366	9	US-11-091-643-19
3	312.2	5.2	4359	9	US-11-091-643-17
4	308.2	5.2	4188	9	US-11-091-643-5
5	307	5.1	3621	7	US-11-058-727-1
6	307	5.1	3621	7	US-11-058-727-1
7	307	5.1	3633	7	US-11-058-727-3
8	307	5.1	3633	7	US-11-058-727-3
9	307	5.1	4874	7	US-11-058-727-17
10	307	5.1	4874	7	US-11-058-727-17
11	307	5.1	6613	7	US-11-058-727-18
12	307	5.1	6613	7	US-11-058-727-18
13	301	5.0	4119	7	US-11-070-575-4
14	152.8	2.6	402	9	US-11-091-643-1
15	87.8	1.5	1860	7	US-11-058-727-15
16	87.8	1.5	1860	7	US-11-058-727-15
17	87.8	1.5	1863	7	US-11-058-727-19
18	87.8	1.5	1863	7	US-11-058-727-19
19	87.8	1.5	2010	7	US-11-058-727-11
20	87.8	1.5	2010	7	US-11-058-727-11
21	87.8	1.5	2019	7	US-11-058-727-57
22	87.8	1.5	2019	7	US-11-058-727-59
23	87.8	1.5	2019	7	US-11-058-727-89

ALIGNMENTS

RESULT 1

US-11-091-643-3

; Sequence 3, Application US/11091643

; Publication No. US20050246789A1

; GENERAL INFORMATION:

; APPLICANT: TANAKA, Masao

; APPLICANT: YOKOYAMA, Tomoko

; APPLICANT: AOYAGI, Moriochi

; APPLICANT: HASEGAWA, Makoto

; APPLICANT: EHARA, Gaku

; APPLICANT: KIMURA, Masaharu

; APPLICANT: NISHIHASHI, Hideji

; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and

; FILE REFERENCE: OP1335

; CURRENT APPLICATION NUMBER: US/11/091,643

; PRIOR FILING DATE: 2005-03-29

; PRIOR APPLICATION NUMBER: JP 2001-115754

; PRIOR FILING DATE: 2001-04-13

; PRIOR FILING DATE: 2001-07-04

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 4359

; TYPE: DNA

; ORGANISM: Bacillus popilliae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (282)...(4229)

US-11-091-643-3

Query Match 6.5%; Score 390; DB 9; Length 4359;

Best Local Similarity 58.0%; Pred. No. 2.7e-73;

Matches 815; Conservative 0; Mismatches 535; Indels 54; Gaps 5;

QY 2292 AATAAGCGAAAAAGGTTGTGAGTCCTATCTTTACAGTAGTAGCAAAAAATACCTTAAAAA 2351

DB 2320 AAAAAGCAAGGAAGCGGTGAACCACTTTCTTACAGTAGTAGCAAAAAAGGCGCTAAAG 2379

QY 2352 TAGAAGCGACAGTTATGAATAGATCAAGCGCCATTCTTATAGATGTATCTCAGATG 2411

DB 2380 AAGGCACGACCGCATTTATGATCGATCAAGCGCCCAACGTGGTGGATTTGTATTCGATG 2439

QY 2412 AACAAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAACTGGAACCAACTTA 2471

Sequence 91, Appl

Sequence 57, Appl

Sequence 58, Appl

Sequence 89, Appl

Sequence 7, Appl

Sequence 21, Appl

Sequence 25, Appl

Sequence 23, Appl

Sequence 43, Appl

Sequence 49, Appl

Sequence 67, Appl

Sequence 69, Appl

Sequence 75, Appl

Sequence 81, Appl

Sequence 7, Appl

Sequence 21, Appl

Sequence 25, Appl

Sequence 29, Appl

Sequence 33, Appl

Sequence 43, Appl

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QY	2472	GTCAAGTCTCGTAACTACTCTCAAAATGGAGACTTTTCT	2509
Db	2497	GCCAGCCGCAATTTACTGCTCAATGGAAATTCGATGATCTATATCCAGCTCTGGAGA	2556
QY	2510	--GGGAATGATTGGACATTTGGTAAATGATATATCATAGGATCCAATAATCTCTATTTT	2567
Db	2557	GGGAGAATCCATGGAAAAAAGTCCGCGATGTTACGATCCGTCAAGATAACCCGATTTT	2616
QY	2568	AGGAAAAATTTCTACAGATGCGTGGAGCAGGACATATATGGAAC-----TCTATTTC	2621
Db	2617	AGGGCCATTATCTCAGTATGGGGGTGCGAAGCATATGAGGCCACCAATGATACCTCC	2676
QY	2622	CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAATAAACCATATACACGTTATCGAG	2681
Db	2677	CCACGTATGCTATCAAAAAATAGACGAGCCAAATTAAGCCATATACCGGTATAAG	2736
QY	2682	TAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGGTAAACACGTTACGGGAAAG	2741
Db	2737	TGCGCGGGTTTGTGTAGCAGCAAGCTCTAGAGCTGTGGTTACACGCTATAATGAAG	2796
QY	2742	AAATTGATCGTATCATGAATGTTCCAAATGATTTGGCCCTATATGAGCCCTAATCTTCAAT	2801
Db	2797	AAATCGATCGATTTTGTAGATGTACCGGATAATATCCGATGCGCGACTCTCTGTCTGG	2856
QY	2802	GTGGAGATTATCGCTGTGAATCATCTGC-----TCAGTATGTGAGCAAG	2846
Db	2857	GTGAATTTGATCGATCGACCCCTATTTGATATCCACTTTACTTCCAGATGTAAACCTG	2916
QY	2847	GGTATCCTACACCAACAGATGGATATGCTCCGATATGATGCATCCGCCCAAAATPATAG	2906
Db	2917	AGTTTATAATCAGATGCAACCATCTCTTGCCACCACCAATCAGATGGTCGATTAACA	2976
QY	2907	ATAGAAGATGTGAAGTGTACAGTCTGTCATCATCTTGAATTTTATATGTACACCGGAG	2966
Db	2977	ACAGAAAAACCCCAAAATGTCAATCAAGCGCATCAATTTGAGTTCCATATTTGATACCGGA	3036
QY	2967	AAATAGATACAAATAGTAAATGATGATGCTTTATTAATAAATTTCTAATCCAGATG	3026
Db	3037	CAATCGATCTGGTCGAAGATTTGGGCATTTGGGTGATCTTCAAAATCTGTGCCACAGATG	3096
QY	3027	GATACGCTCAGTAGGGAATCTAGAAGTCAATTGAAGAAGCACCTAACAGGTGAAGCAT	3086
Db	3097	GTACCGAAGCTTAGATGATTTGGAAGTATTGAAGAAGGCGCTGGGTGTGGAAGCAT	3156
QY	3087	TGGCAGATGTGAACAAAGGAAGAAATGGAACCAACATGGAAGAAACGTTGGG	3146
Db	3157	TAGAACTTGTCAAGAAAAAGAAAAATGGAGACATCAGAAGGAGCAGCATGTGTCGC	3216
QY	3147	AAACAAACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGATTAATTTACAAA-----	3201
Db	3217	AAACGAAACAAATATGATCGGCCCAACACACGCGTGTGGGTATTTCACAAACACGC	3276
QY	3202	-TGAACAAGAGTTTACATATATTTACTTTAGATCATATTTCAAAACGCTGTGCTGCG	3260
Db	3277	GCTATGAAAAATTTGAAGTTTGAACCAACCATCTCCAAATATTTGTATGCTGATCATCTCG	3336
QY	3261	TACAGTCGATTCCTATGATATACCAATTTGGTTACCGAATGCTCCAGGTATGAACTATG	3320
Db	3337	TGCAAGTCGATTCCTATGATATATAAATAATATGATCCGGAAGTTCCAGGTATGAAATTCG	3396
QY	3321	ATGTATATCAAGAGTTTAAACGACGCTATCATGCAAGGTTATATTTATATGATGACGAA	3380
Db	3397	AACTCTATACAGAGCTAAACACTCTGTTCCAGATGCGTTCATCTATATGACCAGGA	3456
QY	3381	ATGTCATAACAAATGTTGACTTTTACACAAGGATTAACGGATGGCAGCAACAGGAAATG	3440
Db	3457	ATCTGATTAATAATGGCGCGCTTTAGCAATGGGCTTATGATTTGGCAGGCTACCCCGCATG	3516
QY	3441	CCGCGGTACAAACAAATGGATGGAGCTTCAGTATTTAGTTTCTATCAAAATGGAGCGCGGG	3500
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QY	3501	TATCTCAAAACTTGCATGCTCAAGATCATCATGGATATGTGTACTGCTGTGATTCGCAAAA	3560
Db	3577	TGTCCAGAGATCTTTGTATCGAACACATCGCGTTATGTATTGCTGTACACGGCGAGA	3636
QY	3561	AAGAAGGACCTGGAAAAAGGTATGTAAACGATGATGATGATTTGAAAGCAAGGAACAC	3620
Db	3637	AAGAAGATCCGGAGCTGGCAATGTACTCTTCAGTGACTGTGCAAAACCATGTGCAACAGC	3696
QY	3621	TTAAGTTTCACTTCTTTCGCAAGAG	3644
Db	3697	TGAGCTTACTTCTTTCGCGATATAG	3720
RESULT 2			
US-11-091-643-19			
; Sequence 19, Application US/11091643			
; Publication NO. US20050246789A1			
; GENERAL INFORMATION:			
; APPLICANT: TANAKA, Masao			
; APPLICANT: YOKOYAMA, Tomoko			
; APPLICANT: AOYAGI, Morichi			
; APPLICANT: HASEGAWA, Makoto			
; APPLICANT: EHARA, Gaku			
; APPLICANT: KIMURA, Masaharu			
; APPLICANT: NISHIHASHI, Hideji			
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or			
; TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and			
; TITLE OF INVENTION: polynucleotide encoding the same			
; FILE REFERENCE: OPI335			
; CURRENT APPLICATION NUMBER: US/11/091,643			
; CURRENT FILING DATE: 2005-03-29			
; PRIOR APPLICATION NUMBER: JP 2001-115754			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: JP 2001-203463			
; PRIOR FILING DATE: 2001-07-04			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 19			
; LENGTH: 4366			
; TYPE: DNA			
; ORGANISM: Bacillus popilliae			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (224)..(4255)			
US-11-091-643-19			
Query Match 5.3%; Score 318.6; DB 9; Length 4366;			
Best Local Similarity 55.7%; Pred. No. 3.8e-58;			
Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;			
QY	2292	AATAAGCGAAAAAGTTGTGAGTCTCTATGTTTACAAAGTAGTACGAAAAATACGTTAAAAA	2351
Db	2196	AAAAAGCAAGAAAGCGGTGAACCAATTTGTTTACAGATGATCGAAAAAGCGCTTAAAG	2255
QY	2352	TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCATAGAAATGTATGTCCAGATG	2411
Db	2256	AAGACACGACCGATTATGAGATTGATCAAGCGCCAAACGTTGATGTTATATCGGATG	2315
QY	2412	AACAAAAATCCTCAGAAAAAATAATGTTATGGGATGAATAAATACTGGCAAAACACTTA	2471
Db	2316	---AGTGTGGACATGATAAATGATCTCTGTTAGATGAAGTAAATATGCAAAACCACTCA	2372
QY	2472	GTCAAGTCTGTAATCTACTCCAAAATGGAGACTTTTCT-----	2509
Db	2373	GCCAGCCGCAATTTTACTGCTCAATGGGAATTCGATGATCTATATTCAGCTCTGGAGA	2432
QY	2510	--GGGAATGATTGGACATTTCCGGTAATGATATTTATCATAGGATCCAATAATCTCTATTTT	2567
Db	2433	AGGAGAAATCCATGGAAAAAAGTCCGAATGTTACGATCGCAAGATAACCCGATTTT	2492
QY	2568	AGGAAAAATTTCTACAGATGCGTGGAGCAGGACATATATGGAAC-----TCTATTTC	2621

Db 2493 AAGGCCATTATCTCAGTATGCGCGGTGCGAACGATATCGAGGCCACCAGTATACCTTCC 2552
QY 2622 CAACCTATATCTGTCACAAAATAGATGAGTCTAAATTAACCAATATACACGTTATCGAG 2681
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QY 2682 TAAGAGGGTTTGTGGGAAGTAGTAAGATTTGAAATTTAAATGTTAAACACGTTACGGGAAAG 2741
Db 2613 TCGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTGGTTTACACGCTATAATCAAG 2672
QY 2742 AAATTGATGATCATGATGTTCCAAATGATTTGGCCTATATGCGCCTTAATCCTTCAT 2801
Db 2673 AAGTTGATGCGATTTAGATGTACCGGATTAATATCCGCAATGCGCGGACTCTCTGTCTGCG 2732
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QY 2835 -----ATGTGAGCCAAAGGGTATCTCTACACCAACAGATGGAT----- 2870
Db 2793 AGTTTATAATCAGATGCAACCTCTCTTGCCACCAATCAGATGGTCTGATTACANTA 2852
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QY 3060 AGAAGGACCATTAACAGGTGAAGCATTCGCATGTGAACAAAGAAAGAAAGAAATGGA 3119
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QY 3120 AACACACATGGAAGAAAACGTTGGAAACACAAACAGCCTATGATCCAGCAAAACAGG 3179
Db 3153 GACATCAGAAGGACGACACTGTTCCAAACGAAACACAAATATGATGGCGCAACATG 3212
QY 3180 CTGTAGATGATTTTACAAATGAAC-----AAGAGTTACACTATCATATTACTTTAG 3233
Db 3213 CGGTGATGGCTTATTTTACAAACAGCGCTATGAAAAATTTGAAGTTTGAACCAACCATTT 3272
QY 3234 ATCATATTCAAAACGCTGATCGACTGGTACAGTTCGATTCCTATGTATACCATTAATGGT 3293
Db 3273 CTGACATTTTGTATGCTGATCATCTCGTGCGGTCGATTCCTTATGTATATAATAATG 3332
QY 3294 TACCGAATGCTCCAGCTATGAACATGATGATATCAAGAGTTTAAACGACGATCATGTC 3353
Db 3333 TACCGAAGTTCCAGGTATGAATTAAGAACTTATTCAGAGCTTAACACACTGGTTTCA 3392
QY 3354 AAGGTTTAAATTTATGATGACGAAATGTCTATAACAAATGGTGACTTTTACACAGGAT 3413
Db 3393 ATCGGTTCTACCTGTATGACAGCGGAATCTGATTAATAATGGCGCTTTAGCAATGGCG 3452
QY 3414 TACAGGATGGCAGCAACAGGAAATGCGCGGTACAAACAAATGGATGGAGCTTCAAT 3473
Db 3453 TTATGATTTGGCAAGCTACTCTCTCATGCAAGATAGAGCAAGAAATATGAGAAATCGGTGC 3512
QY 3474 TAGTTCTCATCAAAATGGAGCGCGGGTATCTCAAAATTTGCAATGCTCAAGATCATCATG 3533
Db 3513 TCGTGTCCAAATTTGGGATGCCAATGTGTGCGAAGATCTTTGTATCGAACAAATCGCG 3572
QY 3534 GATATGTGTGATGTGATTTGCCAAAAAGAGGACCTTGGAAAAGGGTATGTAAACGATGA 3593

Db 3573 GTTATGTTATGCGTGTACGGCGAGAAAAGAGATCCGGAGCTGGCAATGTTTACCTTTA 3632
QY 3594 TGAATTTGTAATGAAAGCAGGAAACACTTAAGTTTCACTTCTTTCGGAAGAAG 3644
Db 3633 GTGACTGTGAAATCATGTCGACAAAGCTGAGCTTTACTTCTTCGATATAG 3683

RESULT 3

US-11-091-643-17
; Sequence 17, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (250)..(4245)
US-11-091-643-17

Query Match 5.2%; Score 312.2; DB 9; Length 4359;
Best Local Similarity 55.5%; Pred. No. 8.6e-57;
Matches 827; Conservative 0; Mismatches 523; Indels 141; Gaps 6;
QY 2292 AATAGCGAAAAGTTGTGAGTCTCTATGTTTACAAGTAGTAGCAAAAATACGTTAAAAA 2351
Db 2186 AAAAAAGCAAGAAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAAAGCGCTAAAG 2245
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGTATGTCAGATG 2411
Db 2246 AAGACACGACCGATTATGAGATTGATCAAGCGCCACCGTTGTTATATCGGATG 2305
QY 2412 AACAAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2306 ---AGTGTGGACATGAGAAAAATGATCTCTGTAGTGAAGTAAAAATATGCAAAACAACTCA 2362
QY 2472 GTGAGTCTGTTAATCTACTCCAAAATGGAGACTTTTCT----- 2509
Db 2363 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTTTCGATGATCTATATCCAGCTCTCGAGA 2422
QY 2510 ---GGGAATGATTGGACATTCGGTAAATGATATTATCATAGAGTCCCAATAATCCTATTTTTA 2567
Db 2423 GGGAGATCCATGGAAAACAACTCGAATGTTTACGATCGTCAAGATAACCCGATTTTAA 2482
QY 2568 AAGGAAAAATTTCTACAGATGCGTGGGACGACGAGACATATATGGAAC-----TCTATTTC 2621
Db 2483 AAGGCCATTATCTCAGTATGGCGGTGCGAACGATATCGAGCCCACTATGATCGTTCC 2542
QY 2622 CAACCTATATCTGCAAAAATAGATGAGTCTAAATTAATAAACCATATACACGTTATCGAG 2681
Db 2543 CCACGATGCTCTATCAAAAATAGATGAAGCCCAATTAAGCCCATATACACGTTATAAG 2602
QY 2682 TAAGAGGGTTTCTGGGAAGTAGTAAAGATTTCGAAATTAATGTTAACACGCTTACGGGAAG 2741

Db 2603 TCGCGGGTTGTGGCAGCAGCAAGATCTGAGCTGTGGTATACACGCTATAATGAAG 2662
Qy 2742 AAATTGATGCTATCATGATGTTCCAAATGTTGGCTTATATGACAGCCTAATCTTCAT 2801
Db 2663 AAGTTGATCGGATTTAGATGTACCGGATAATATCCGCATGCGCGACTCTCTGTCTGG 2722
Qy 2802 GTGGAGATTACGCTGTGTGAATCATCTCTCA -----TGCTCCG 2879
Db 2723 GTGAATTTGATCGATCGAAGCCCTATTCTGTATCCACCTTTACTTCCAGAAATGTAACCCCTG 2782
Qy 2833 -----GTATGTAGCCAGGATCTCTACCAACAGATGGATA----- 2871
Db 2783 AGTTTATAAATCAGATGCAACCATCTCTTGGCACCACCAATCAGATGTCGATTAACAATA 2842
Qy 2872 -----TGCTCCG 2879
Db 2843 ACATGAAACAGGACGAGTACTACCATGAATCCTAGCATGAATCTCTCCCTTACGCCCTG 2902
Qy 2880 ATATGTATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACAGATCGTCATC 2939
Db 2903 AAATAGCATCCAGCCAAAGTGGATTCCGCAGAAAACATCGCAATGTCTCAAGCGCATC 2962
Qy 2940 CATTTGATTTTCATATTGACACCGGAGAGTAGATACAATGTAGTATGATG 2999
Db 2963 AATTTGAGTTCACATTTGATACCGGACCAATCGAATTTGGTGAAGATTTGGGCATTTGGG 3022
Qy 3000 TCTTATTAATAATTTCTAATCCAGATGGATACCTACAGTAGGAACTTAGAAGTCATG 3059
Db 3023 TGATCTTCAAAATCTGTGCCACAGATGGATACGCAAGCTTAGATGTCTGGAAGTATG 3082
Qy 3060 AAGAAGGACCTAAACAGGTGAAGCATTTGGCAGATGTGAAACAAAGAAAGAAATGGA 3119
Db 3083 AAGAAGGAGCGTGGGGTGGAGCCTTAGAATCTTCAAGAAAAGAGAAAAGAAATGGA 3142
Qy 3120 AACACACATGAGAAAAGAAAGTGGGAAACACAAACAGCTTATGATCCAGCAAAACAGG 3179
Db 3143 GACATCAGAAGGAGCAGCACTGTTCGCAACGAAACACAAATATGATGCGGCCAAACATG 3202
Qy 3180 CTGTAGATGCTATTTTACAAA-----TGAAACAGATTTACACTATCATTTACTTTAG 3233
Db 3203 CGGTGATGGGTTATTTACAAACCGGCTATGAAAAATTTGAATTCGAAACAAACCATTT 3262
Qy 3234 ATCATATTCAAAACGCTGATCGACTGGTACGTCGATTCCTTATGTATACCATTAATGTT 3293
Db 3263 CTGACATTTTGTATGCTGATCATCTCTGTCAGTCGATTCCTTATGTATATAATAATG 3322
Qy 3294 TACCGAATGCTCCAGGTATGMACTATGATGTATATCAAGATTTAAACGCAAGTATCATGC 3353
Db 3323 TACCGGAAGTTTCAGGTATGAATTTACGAACTCTATACAGAGCTAAACACTCTCGTTTCA 3382
Qy 3354 AAGGTTATTAATTTATATGATGCACAGAAATGTCTATAACAAATGGTGTACTTTACACAGGAT 3413
Db 3383 ATGCGTTCTACCTGTATGACCGGAAATCTGATTAATAATGGCGCTTTAGCAATGGCG 3442
Qy 3414 TACAGGATGGCAGCAACAGGAAATCCCGCGGTACAAACAAATGGATGGAGCTTCAGTAT 3473
Db 3443 TTATGTATTGGCAAGCTACCCGCAATGACAGAGTGGAGCAAGAAATATGATAGATCAGTGC 3502
Qy 3474 TAGTTCTATCAATTTGGAGCGGGGTATCTCAAACTTGCATGTCTCAAGTATCATG 3533
Db 3503 TGGTGTCCGGAATTTGGGATGCAATGTGTGCAACAGCTGTGTATCGAACACAATTCGCG 3562
Qy 3534 GATATGTGTACGTGTGATTGCCAAAAAGAGGACCTCGAAAAGGGTATGTAACGATGA 3593
Db 3563 GTTATGTATTGGTGTTCACGGCGAGAAAGAGATCCGGAGCGCGCAATGTTACCTTTA 3622
Qy 3594 TGGATTGTAAAGGAGGAGAAACCTTAAGTTTCACTTCTTTCGGAAGAG 3644
Db 3623 GTGACTGTGCAAAATCATGTGCAACAGCTGAGCTTTACTTCTTCGATATAG 3673

US-11-091-643-5
; Sequence 5, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morilchi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4188
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4158)
US-11-091-643-5

Query Match 5.2%; Score 308.2; DB 9; Length 4188;
Best Local Similarity 55.2%; Pred. No. 6e-56;
Matches 817; Conservative 0; Mismatches 533; Indels 129; Gaps 6;

Qy 2292 AATAAGCGAAAAAGTTGTGAGTCTCTATGTTTCAAGTAGTACGAAAAATACGTTAAAAA 2351
Db 2066 AAAAAAGCAAGGAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAAAGGCGCTAAAAA 2125
Qy 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCATTTCTATAGAAATGTATGCAGATG 2411
Db 2126 AAGGCACGACAGATTATGAGATCGATCAAGCGCCCAACGTTGTTATATCGATG 2185
Qy 2412 AACAAAAATCCTCAGAAAAAAATAATGTTATGGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2186 ---AGTGTGGACATCAGAAAAATGATCCTGTTGGATGAAGTGAATATGCAAAACAACTCA 2242
Qy 2472 GTGAGTCTGTTATCTCTCCAAAATGGAGACTTTTCT----- 2509
Db 2243 GCCAAGCCGCAATTTACTGCTCAATGGGAATTTTCGATGATCTATATCCAGCTCTGGAGA 2302
Qy 2510 ---GGGAATGATTGGACATTTCCGTTAATGATATTATCATAGGATCCAAATATCTATTTTA 2567
Db 2303 GGGGAATCCATGGAAAAACAGCCCGAATGTTTACGATCCGTCAAGATAACCCGATTTTA 2362
Qy 2568 AAGGAAAAATTTCTACAGATGCGTGGAGCAGCAGACATATATGGAAC-----TCTATTTTC 2621
Db 2363 AAGGCCATTTATCTCAGTATGGCGGTGCGAACGATATCGAGGCCCAATGATACCTTCC 2422
Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAATAACCATATATACACGTTATCGAG 2681
Db 2423 CCACGTATGCTTATCAAAAAATAGACGAAGCCAAATTAAGCCGTATATACACGTTATAAG 2482
Qy 2682 TAAGAGGGTTTCTGGGAAGTAGTAAGATTTTGAATTAATGTTAAACACGTTACGGGAAAG 2741
Db 2483 TCGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTTGGTTACACGCTATATGAAG 2542
Qy 2742 AAATGATGCTATCATGAATGTTCCAAATGATTTGGCCCTTATATGAGCCCTAAATCTTCAT 2801
Db 2543 AAGTCGATCGGATTTTAGATGTACCGGATAATATCCCGCATGCGCGGATACCTGTCGCG 2602
Qy 2802 GTGGAGATTATCGCTGTGTAATCATCGTC-----TCAGTATGTAGCCAA 2845


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Db 2543 GT-----ATCAATCGATGCGAGCAAAA 2567
QY 2880 ATATGATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGTCTGTCATC 2939
Db 2568 GTATGTGAATAGCGGTTTAGAAGTAGAAAAACCGTCTCTGGTGAAGCG-----CATG 2617
QY 2940 CATTTGATTTTCATATTGACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATG 2999
Db 2618 AGTTCTCTATTCTTATTTGATACAGGTGAAATCGAATTCGAATTAATGAAATGCAAGNAATGGG 2677
QY 3000 TCTTATTAATAAATTTCTTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAGTCAATG 3059
Db 2678 TTGGATTAAAGATTACGGACCCAGAGGATATGCAACATCTCGAAACCTTAGAATTGGTGG 2737
QY 3060 AAGAAGGACCTTAACAGGTGAAGCATTTGGCACAATGTGAAACAAAAAGGAAGAAATGGA 3119
Db 2738 AAGAGGGACCTTTATCAGGAGACGCATTAGAACGCTTGCAAGAGAGAAGAACACAGTGG 2797
QY 3120 AACACACATGGAGAAAAACGTTGGGAAACACAAACAGCCTATGATCCAGCAAAACAGG 3179
Db 2798 AGATTCAAAATGCAAGAAGACGTAAGAAACACAGATAGAAAGGTATATGGCATCGAAACAAG 2857
QY 3180 CTGTAGATGATTATTTACAAATGAAACAAGAGTTACACTATCATATTAATTTAGA----- 3234
Db 2858 CGGTAGATCGTTTATATGCGATTATTCAGGATCAGCAACTGAATCTCTGATGTAGAGATTA 2917
QY 3235 -TCATATTCAAAACGCTGATCGATCGGTACAGTCGATTCCTTATGTATATACCAATATGGT 3293
Db 2918 CAGATCTTACTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATTAACGAATGT 2977
QY 3294 TACCGAATGCTCAGGTATGAACATATGATGTATATCAAGATTAAACGACGCTATCATGC 3353
Db 2978 TCCAGAAATACACAGGGTGAACATATACGAAGTTTACAGAATTAACAGATCGCACTCCAAC 3037
QY 3354 AAGGTTATATTTATATGATGCACGAAATGTCAATCAAAATGTGTGACTTTTACACAAGGAT 3413
Db 3038 AAGCGTGGAGTTTGTATGATCAGCGAATGCCATACCAATGGTGTATTTTCGNAATGGGT 3097
QY 3414 TACAGGGATGGCACGCAACAGGAAATGCCCGGTACAAACAAATGGAAGTTCAGTAT 3473
Db 3098 TAAGTAATTTGGAATGCAACGCTTGGCGGTAGAAAGTTCACAAATCAATCATCATCTGTCC 3157
QY 3474 TAGTTCTATCAANTTGGAGCGGGGTATCTCAAAATTCGATGCTCAGATCATCATG 3533
Db 3158 TTGTGATTCCAAATCGGATGAGCAAGTTTCGCAACAGTTTACAGTTTCAACCGGAATCAA 3217
QY 3534 GATATGTGTATCGTGTGATTTGCCAAAAAGAGGACCTTGGAAAAAGGTATGTAAACGATGA 3593
Db 3218 GATATGTGTACAGTTACTGCGAGAAAGAGGGGTAGGAATGGATATGTAAATATCC 3277
QY 3594 TGAATTGTAATGAAAGCAGGAAACACTTAAGTTCACTTCTTTCGGAAGAG 3644
Db 3278 GTGATGGTGGAAATCAACAGAAACGCTTACTTTTAGTGAACGATTATG 3328
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RESULT 6

US-11-108-389-1

; Sequence 1, Application US/11108389

; Publication No. US20050261188A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Presnail

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; TITLE OF INVENTION: Activity

; FILE REFERENCE: 35718/291049

; CURRENT APPLICATION NUMBER: US/11/108,389

```
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-1
US-11-108-389-1
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Query Match 5.1%; Score 307; DB 7; Length 3621;

Best Local Similarity 55.7%; Pred No. 1e-55;

Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;

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QY 2292 AATAAGCGAAAAAGGTGTGTAGTCTCTATGTTTACAAGTAGTAGTACGAAAAATACGTTAAAAA 2351
Db 2018 AAGCAGCGAAGAAAGACAGTGAATGCTTGTGTTTAC--GAATACAAAAGATGGCTTACGAC 2074
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCATAGATGATGTATGTCAGATG 2411
Db 2075 CAGGCGTAACCGATTATGAAGTGAATCAAGCGGCAAACTTAGTGAATGCCCTATCGGATG 2134
QY 2412 AACAAAACTCTCAGGAAAAATAAATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2135 ATTTGTATCCAAATGAAAAACGATTGTTATTTGATGCACTGAGAGGCGAAAAACGCTCA 2194
QY 2472 GTCACTGTCTGAATCTACTCCAAAATGGAGACTT-----TTCTGGGAATGATT 2519
Db 2195 GTGAGCAGGTAATTTGCTTCAAGATCCAGATTTCGAAGAGATAAAATGGAGAAAAATGGCT 2254
QY 2520 GCACATTCCGTTAATGATATATTCATAGGATCCAATAAATCCTATTTTAAAGGAAAAATTC 2579
Db 2255 GACGCGCAAGTACGGGAATTGAGGTTATAGAAAGGGATGCTTTATTTCAAAGGCGGTTATC 2314
QY 2580 TACAGATGCGTGAGCAGACAGACATATATGGAACCTCTATTTCCAACTATATCTGTCAA 2639
Db 2315 TACGCTTACCAGTGGAGAGAAATAGATACGGAACGTTATCCAAGTATCTGTATCAA 2374
QY 2640 AAATAGATGAGTCTAAATTTAAAAACCATATACAGTTTTCGATTAAGAGGGTTTGTGGGAA 2699
Db 2375 AAGTAGAGGAAGGTGTATTTAAAAACCATACACAAGATATAGATTGAGAGGGTTTGTGCGAA 2434
QY 2700 GTAGTAAAGATTGAAATTAATGTTAAACAGCTTACGGGAAAGAAATGTATGCTATCATGA 2759
Db 2435 GCAGTCAAGGATTGGAATTTTCACAATTCGTCA-----TCAACGAACCGAA 2482
QY 2760 ATGTTTCCAAATGATTGGCCTATATGCAAGCCTAAATCCTTCAATGTGGAGATTATCGCTGTG 2819
Db 2483 TTGTAAAAAATGTACCGGATGATTGCTGCCAGATGTATCTCTCTGTTAACTCGGATGTA 2542
QY 2820 AATCATCGTCTCAGTATGTGAGCCCAAGGATATCCTACAAACAGATGATGTCTCCCG 2879
Db 2543 GT-----ATCAATCGATGCGAGCAAAA 2567
QY 2880 ATATGATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGTCTGTCATC 2939
Db 2568 GTATGTGAATAGCCGTTTAGAAAGTAGAAAAACCGCTTCTGGTGAAGCG-----CATG 2617
QY 2940 CATTTGATTTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATG 2999
Db 2618 AGTTCTCTATTCTTATTTGATACAGGTGAATCGATTACAAATGAAATGCAAGNAATGGG 2677
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3120	Qy	AACAAACATGGAGAAAAAAGCTTTGGGAAACACAAACAGCCTATGATCTCCAGCAAAACAGG	3179
2810	Db	AGATTCAAATGACAGAGAGCGTGAAGAAAAACAGATAGAAAGGTATATGGCATTCGAAAAACAG	2869
3180	Qy	CTGTAGATGCATTATTTACAAATGAAACAGAGATTACACTATCATATTACTTTTAGA-----	3234
2870	Db	CGGTAGATCGTTTATATGCCGATTTATCAGGATCAGCAACTGTAATCTCGATGTAGAGATTATTA	2929
3235	Qy	-TCATATTCAAAACCGCTGATCGACTGTGACAGTGCATTCCTCTATGTTATACATAATTGGT	3293
2930	Db	CAGATCTTACTTCGGCGCCCAAGATCTGATACAGTCCATTCCTTTACGTATATAAACGAAATGT	2989
3294	Qy	TACCGAATGCTCCAGGTTATGAACATCATGATGTATATCAAGAGTTTAAACGACAGTATCATGC	3353
2990	Db	TCCCAGAAATACCAAGGAGTGNACTATACGAAAGTTTACAGAAATTAACAGATCGACTCCAAC	3049
3354	Qy	AAGGTTATAATTATATGATGCACGAAATGTCATAACAAATGGTGACTTTTACACAAAGGAT	3413
3050	Db	AAGCGTGGAGTTTGTATGATCAGCGAAATGCCATACCAAATGGTGTATTTTCGAAATCGGT	3109
3414	Qy	TACAGGGATGGCAGCGCAACAGGAAATGCGCGGTACAAACAAATGGATGGAGCTTTCAGTAT	3473
3110	Db	TAAGTAATTGGAATGCAACGCGCTGGCGTAGAAGTACAAACAAATCAATCATCATCTGTCC	3169
3474	Qy	TAGTTCTATCAAATTTGAGCGCGGGGTATCTCAAAACTTGTCATGCTCAAGATCATCATG	3533
3170	Db	TTGTGATTCCAAACTGGGGATGAGCAAGTTTCGCCAACAGTTTTACAGTTTCAACCGGAATCAAA	3229
3534	Qy	GATATGTTTACGTGTGATTGCCAAAAAAGAGGACCTGGAAAGGGGTATGTATACGATGA	3593
3230	Db	GATATGTGTACGAGTTACTGCGAGAAAGAGAGGGGTAGGAATGGATATGTATAGTATCC	3289
3594	Qy	TGGATTGTAATTGGAAACGAGAAACACTTAAGTTTCACCTCTTTCGCAAGAAAG	3644
3290	Db	GTGATGGTGGAAATCAAAACGAAACGGTTACTTTTGTAGTGAAGCGCATATG	3340

RESULT 8

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US-11-108-389-3
; Sequence 3, Application US/11108389
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3633
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3633)
; FEATURE:
; NAME/KEY: misc feature

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Db 2930 CAGATCTTACTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATAACGAAATGT 2989
Qy 3294 TACCGATGCTCAGGATGAACTATGATGATATCAAGAGTTAAAGCGACGATCATGC 3353
Db 2990 TCCAGAAATACAGGAGTAACTATACGAAATTTACAGAAATTAACAGATCGACTCCAAC 3049
Qy 3354 AAGGTTATATATGATGACGAAATGTCAACAAATGTCAAAATGGTGTGACTTTACACAAAGGAT 3413
Db 3050 AAGCGTGGATTTGTATGATCAGGAAATGCCATCAAAATGGTGTGATTTTCGAAATGGGT 3109
Qy 3414 TACAGGATGGCAGCAACAGGAAATGCCCGGTACAAACAAATGGATGGAGCTTCAGTAT 3473
Db 3110 TAAGTAATGGAATGCAACGCTGGGTAGAAAGTACAAACAAATCAATCATACATCTGTCC 3169
Qy 3474 TAGTCTCATCAATTTGGAGCGGGGTATCTCAAACTTCGATGCTCAAGATCATCATG 3533
Db 3170 TTGTGATTCCAAACTGGGATGAGCAAGTTTCGCAACAGATTTACAGTTCAACCGAATCAAA 3229
Qy 3534 GATATGTTTACGTGTGATTCGCAAAAGAGGACCTGAAAAGGTATGTAACGATGA 3593
Db 3230 GATATGTTTACGATTTACTGCGAAGAAAGAGGGGTAGGAATGATATGTAAGTATCC 3289
Qy 3594 TGAATGTAATGAAAGCAGCAACACTTAAGTTCACTTCTTCGGAAGAG 3644
Db 3290 GTGATGTTGGAATCAACAGAAACGCTTACTTTTAGTGAACGATTAAG 3340
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RESULT 9

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US-11-058-727-17
; Sequence 17, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4874
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic DNA 1218-1
US-11-058-727-17
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Query Match 5.1%; Score 307; DB 7; Length 4874;
Best Local Similarity 55.7%; Pred. No. 1.1e-55;
Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;
Qy 2292 ATAACGGAAGGTTGTGAGTCTTATGTTTCAAGTAGTAGCAAAATACGTTAAAAA 2351
Db 2748 AAGCAGGAGAAAGCAGTGAATGCCTTGTGTAC---GAATACAAAGATGGCTTACGAC 2804
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Qy 2352 TAGAAACGACAGATTAATGAAATAGATCAAGCGGCCCAATTTCTTATAGAAATGTATGTCAGATG 2411
Db 2805 CAGCGCTAACGATTAATGAAATAGATCAAGCGGCCCAATTTCTTATAGAAATGCCTATCGATG 2864
Qy 2412 AACAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2865 ATTTGTATCCAAATGAAAAACGATTTGTTATTTGATGCACTGAGAGAGGCAAAACGCTCA 2924
Qy 2472 GTCACTCTGTAATCTACTCCAAATGGAGACTT-----TTCTGGGAATGATTT 2519
Db 2925 GTGAGGCAGCTAATTTGCTTCAAGATCCAGATTTCCAAGAGATAAATGGAGAAAAATGGCT 2984
Qy 2520 GGACATTCGGTAATGATATTTATCATAGGATCCAATAATCTCTATTTTAAAGGAAAAATTC 2579
Db 2985 GAGCGCAAGTACGGGAATTTAGGTTATAGAGGGGATGCTTTATTTCAAGGGCGTTATC 3044
Qy 2580 TACAGATGCGTGGAGCACGAGACATATATGGAACCTCTATTTCCAACCTATATCTGTCAAA 2639
Db 3045 TACGCCCTACAGGTGCGAGAGAAATAGATACGGAACGATATCCAACGTATCTGTATCAAA 3104
Qy 2640 AATAGATGAGTCTAAATTTAAACCATATACAGTTATCGAGTAAGAGGGTTTGTGGAA 2699
Db 3105 AAGTAGAGGAAGGTGATTTTAAACCCATACACAAGATATAGATTTGAGAGGGTTTGTCCGAA 3164
Qy 2700 GTAGTAAAGATTTGAAATTAATGGTAAACACGTTACGGGAAAGAAATTTGATGCTATCATGA 2759
Db 3165 GCAGTCAGGATTTGGAATTTTCACTATTCGTA-----TCAACGAAACGAA 3212
Qy 2760 ATGTTTCCAAATGATTTGGCTATATGACGCTTAATCCTTATGTTGGAGATTAATCGCTGTG 2819
Db 3213 TTGTAATAAATGTCGGGATGATTTGCTGCCAGATGATATCTCTCTGTTAACTCGGATGGTA 3272
Qy 2820 AATCATGCTCAGTATGTGAGCCAAAGGTATCTTACACCAACAGATGATATGCTCCCG 2879
Db 3273 GT-----ATCAATCGATGCGAGCAACAAA 3297
Qy 2880 ATATGTATGATGATCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACGATCGTCATC 2939
Db 3298 GTATGTGATAGCCGTTTATAGAGTAGAAGAACCGTTCTGTTGAAGCG-----CATG 3347
Qy 2940 CATTTGATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGATGATGATGATG 2999
Db 3348 AGTTCTCTATTCTTATGATACAGGTGAAATCGATTACAAATGAAATGCAAGGATATGG 3407
Qy 3000 TCTTATTAATAATTTCTAATCCAGATGATGATGATGATGATGATGATGATGATGATGATG 3059
Db 3408 TTGGATTTTAAAGTATACGACCCAGAGGGATATGCAACACTCGGAAACCTAGAAATGGTGC 3467
Qy 3060 AAGAAAGGACCACTAACAGGTGAAGCATTTGGCAGATGTGAAACAAAGGAAAGAAATGGA 3119
Db 3468 AAGAGGACCTTTATCAGGAGACGATTTAGAACGCTTGGAAAGAGAGAGAGAGAGAGAGAG 3527
Qy 3120 AACAAACATGAGGAAAAAACGTTGGGAAACAAACAGCCCTATGATCCAGCAAAACAGG 3179
Db 3528 AGATTCAATGACAAAGACGCTGAAGAAACAGATAGAGAGGTATATGGCATCGAAACAAAG 3587
Qy 3180 CTGTAGATGCATTTTCAAAATGAACAGAGTTACACTATCATATTTACTTTTGA----- 3234
Db 3588 CGGTAGATCGTTTATATGCTCGATTTATCAGGATCAGCAACTGAATCCTGTATGATGATTA 3647
Qy 3235 -TCATATTCAAAACGCTGATCGACTGCTGATGCTGATTCCTTATGATATACCAATAATGGT 3293
Db 3648 CAGATCTTACTCGGGCCAGATCTGATACAGTCCATTCCTTACGTTATATACGAATGAT 3707
Qy 3294 TACCGAATGCTCCAGGTATGAACATATGATGATATCAAGAGTTTAAACGCAACGCTATCATGC 3353
Db 3708 TCCAGAAATACAGGAGTGAATATACGAACTTTACAGAAATTAACAGATCGACTCCAAC 3767
Qy 3354 AAGGTTATATTTATGATGACGAAATGTCATTAACAAATGCTGATGATTTTACACAGGAT 3413
Db 3768 AAGCGTGGAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3827
Qy 3414 TACAGGATGGCAGCAACAGGAAATGCCCGGTACCAACAAATGGAATGGATGAGCTTCAATG 3473
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3120	AACAAACACATGGAGAAAAAAGCTTTGGGAAACACAAACAGGCTATGATCCAGCAAAACAGG	3179
4063	AGATTCAATGACAGAGACGCTGAAGAAACAGATAGAGGTATATGGCATCGAAACNAG	4122
3180	CTGTAGATGCATTTATTTACAAATGAAACAGAGTTACACTATCATATTACTTTTAGA	3234
4123	CGGTAGATCGTTTATATGCGGATTTATCAGGATCAGCAACTGTAATCTCTGATGTAGAGATTA	4182
3235	-TCATATTCAAACGCTGATCGACTGGTACAGTCGATTCCTCTATGTATATACCAATTTGGT	3293
4183	CAGATCTTACTGCGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATAACGAAATGT	4242
3294	TACCGAATGCTCCAGGTATGAACATATGATGTATATCAAGAGTTPAAAACGCACGTATCATGC	3353
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3414	TACAGGGATGGCACGCAACAGGAAATGCCCGGTACAAACAAATGGATGGAGCTTCAGTAT	3473
4363	TAAGTAATTTGGAATGAACAGCCTGGCGGTAGAAGTACAAACAAATCAATCATCATCTGTCC	4422
3474	TAGTTCTATCAAAATTTGAGCGCGGGGTATCTCAAAACTTTGCATGTCTCAAGATCATCATG	3533
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3534	GATATGTTTACGTGTGATTTGCCAAAAAGAGGACCTGGAAAAAGGTATGTAAACGATGA	3593
4483	GATATGTTTACGAGTTACTGCCAGAAAAAGAGGGGTAGGAAATGGATATGTAAATATCC	4542
3594	TGATTTGTAATGAAACAGGAAACACTTAAGTTTCACTTCTCTCCGAGAGAG	3644
4543	GTGATGGTGAATCAACACAGAAACGCTTACTTTTAGTGCACGCGATTATG	4593

RESULT 13

US-11-070-575-4

; Sequence 4, Application US/11070575

; Publication No. US20050271642A1

; GENERAL INFORMATION:

; APPLICANT: ASANO, Shin-ichiro

; APPLICANT: NOZAWA, Mikiko

; APPLICANT: BANDO, Hisanori

; TITLE OF INVENTION: RECOMBINANT ORGANISMS PRODUCING INSECT

; FILE OF INVENTION: TOKINS AND METHODS FOR CONSTRUCTING SAME

; FILE REFERENCE: 595622000300

; CURRENT APPLICATION NUMBER: US/11/070, 575

; CURRENT FILING DATE: 2005-03-01

; PRIOR APPLICATION NUMBER: US 60/549, 094

; PRIOR FILING DATE: 2004-03-01

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 4119

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Db 121 TAGCGAAGCTTAGATGATTTGGAAGTGATTTGAAGAAGGAGCGCTGGGTGTGGAAGCATTTA 180
QY 3089 GCACATGTGCAACAAAGGAAGAAATGGAACACACATGAGAGAAAAAGCTTGGGAA 3148
Db 181 GAACTTTGTCAAGAAAAAGAAAAAGAAATGGAGACATCAGAAGGAGAGCACTGTTCCGCAA 240
QY 3149 ACACAAACAGCCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTACAAA-----T 3202
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QY 3203 GAACAAGAGTTACATCATATCATATTTACTTTAGATCATATTCAAAACGCTGATCGACTGGTA 3262
Db 301 TATGAATAAATTTGAAGTTTCAAAACACCACTCTCCAATATTTTGTATGCTGATCATCTCGTG 360
QY 3263 CAGTCGATTCCTCTATCATACCATATTTGTTACCGAATGCT 3304
Db 361 CAGTCGATTCCTTATGATATATAATAATAATATGTACCGGAAGTT 402

RESULT 15

US-11-058-727-15
; Sequence 15, Application US/11058727
; Publication No. US20050261493A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-058-727-15

Query Match 1.5%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 2.4e-09;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;
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Db 555 TAACTATTATGATCGTCAAAATGAAACTTTACTGCAAGAAATATTCTGATCACTGTGTAAAGTG 614
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Db 615 GTATGAAACTGGTTTGGCAAAATTAATA-----GGCAGAGCGCTAAACAATGGGTTCA 668
QY 1001 ATTTTAATAATTTCTAGAGAAATGACGTTGGCGGTATTTGGATATATTGCTATATTTC 1060
Db 669 CTATTAACCAATTCCTGAGAGAAATGACACTGGCGGTTTTAGATGTTTGTTCATTATTCCC 728
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Db 729 AAAATTATGACACACACGACGCTACCCCAATCGAAACGAAAGCACAACTAAACAAGGAAGTATA 788
QY 1121 TACAGATGCGTGGGATATTTCATCGGGAACTTTATAGTTGGTTTACCGAAT 1169
Db 789 TACAGATCCACTGGGCGGTTAAACGTGCTCTTCAATTGGTTCTCGGTAT 837

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Job time : 410.161 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:41:30 ; Search time 683.153 Seconds
(without alignments)
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Title: US-10-781-979-1
Perfect score: 5980
Sequence: 1 tacatgaataacataaag.....ttctaaaaagcctctgtat 5980

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfilese1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	765.8	12.8	3543	3	US-09-224-024-27
2	765.8	12.8	3543	6	PCT-US94-07902-27
3	380.8	6.4	3504	3	US-10-089-678-2
4	380.8	6.4	3690	3	US-10-089-678-3
5	358	6.0	3797	2	US-07-915-203-1
6	358	6.0	3797	2	US-08-272-887-1
7	358	6.0	3797	2	US-08-789-449-1
8	314.6	5.3	3471	2	US-07-876-280-29
9	314.6	5.3	3471	2	US-07-812-180A-1
10	314.6	5.3	3471	2	US-08-315-468-1
11	314.6	5.3	3471	3	US-07-941-650A-1
12	308.2	5.2	3726	3	US-09-001-982-11
13	308.2	5.2	3726	3	US-09-668-650-11
14	305.4	5.1	3414	2	US-07-973-320-3
15	302.2	5.1	3414	2	US-07-973-320-1
16	288.4	4.8	3507	2	US-08-315-468-3
17	278.4	4.7	3759	2	US-08-542-921-1
18	278.4	4.7	3759	2	US-08-880-685-1
19	278.4	4.7	3759	2	US-08-880-684-1
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21	276.4	4.6	3522	2	US-08-291-368-1
22	276.4	4.6	3522	2	US-08-962-190-1
23	276.4	4.6	3522	6	PCT-US95-10310-1
24	276.4	4.6	3522	9	5164180-3

25	275.6	4.6	3468	3	US-09-001-982-9	Sequence 9, Appli
26	275.6	4.6	3458	3	US-09-668-650-9	Sequence 9, Appli
27	275.6	4.6	3471	3	US-09-002-285-71	Sequence 71, Appl
28	275.6	4.6	3471	3	US-09-589-477-71	Sequence 71, Appl
29	275.6	4.6	3471	3	US-10-099-285A-71	Sequence 71, Appl
30	273.2	4.6	3504	3	US-09-661-322A-39	Sequence 39, Appl
31	271.8	4.5	4344	2	US-08-532-547-4	Sequence 4, Appli
32	271.8	4.5	4344	2	US-08-379-656B-4	Sequence 4, Appli
33	271.8	4.5	4344	3	US-08-455-838-4	Sequence 4, Appli
34	271.8	4.5	4344	3	US-09-019-809-4	Sequence 4, Appli
35	271.8	4.5	4344	3	US-09-471-177-4	Sequence 4, Appli
36	271.8	4.5	4344	3	US-09-220-806-4	Sequence 4, Appli
37	270.8	4.5	3453	3	US-09-002-285-75	Sequence 75, Appl
38	270.8	4.5	3453	3	US-09-589-477-75	Sequence 75, Appl
39	270.8	4.5	3453	3	US-10-099-285A-75	Sequence 75, Appl
40	270.2	4.5	3504	2	US-08-291-368-3	Sequence 3, Appli
41	270.2	4.5	3504	2	US-08-962-190-3	Sequence 3, Appli
42	270.2	4.5	3504	6	PCT-US95-10310-3	Sequence 3, Appli
43	270	4.5	3471	3	US-09-002-285-73	Sequence 73, Appl
44	270	4.5	3471	3	US-09-589-477-73	Sequence 73, Appl
45	270	4.5	3471	3	US-09-661-322A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-224-024-27
; Sequence 27, Application US/09224024
; Patent No. 6056953
; GENERAL INFORMATION:
; APPLICANT: Leslie Hickie
; APPLICANT: Jewel Payne
; TITLE OF INVENTION: Materials and Methods for the Control of
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,024
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3543 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-224-024-27
Query Match 12.8%; Score 765.8; DB 3; Length 3543;
Best Local Similarity 71.5%; Pred. No. 2.2e-161;

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07902-27

Query Match 12.8%; Score 765.8; DB 6; Length 3543;

Best Local Similarity 71.5%; Pred. No. 2.2e-161;

Matches 1058; Conservative 0; Mismatches 397; Indels 24; Gaps 3;

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QY 2352 TAGAAACGACAGATTTATGAATAGATCAAGCGGCCATTTCTTATAGAATGTATGTCAGATG 2411
DB 2132 CAGAACTTACAGATTTATGACATAGATCAAGCGCCCAATCTTGTGGAATGTATTTCTGAAG 2191
QY 2412 AACAAATCTCAGGAAATAATAATGTTTATGGGATGAATAAATACTGGCAAAACAACTTA 2471
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DB 2252 GTCNAATCTGAAATGTAATCTCAAAACGGGATTTTGAATCGGCTACCGCTTGGTTGGACAA 2311
QY 2526 TCGGTAATGATTTATCATAGGATCCCAATATCTTATTTTAAAGGAAAAATTTCTACAGA 2585
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QY 3186 ATGCATTTTACAAATGAACAGA-----GTTACACTATCATATTTACTTTAGATCATTA 3239
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QY 3240 TTCAAAACGCTGATCGACTGGTACAGTCGATTCCTATGTATACCAATAATTTGGTTACCGA 3299
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DB 3020 TTCAGTACGCTGAGTATTTGGTACATCGATTCATATGTTGTAATGATGTTGTGCAG 3079
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DB 3080 ATGCTCAGGTATGAATTTATGATATCTATGTAGAGTTGGATGACGAGTGGCAACGCGC 3139
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DB 3320 TCTTACGTGTTATGCGAAAAAAGAGGACCTCGAAATGGGTATGTCACGCTTATGATG 3379
QY 3600 GTAATGGAAGCAGGAAACACATTAAGTTTCACTTTCTTCCGAAAGGATATATGACAAAAA 3659
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QY 3720 CATTTTATATAGATACATCGAGTCTGTTGTATGCAAG 3758
DB 3500 CGTTTTATATCGAAAGCATTTGAATTAATTTGTCATGAACG 3538
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RESULT 3

US-10-089-678-2

; Sequence 2, Application US/10089678

; Patent No. 6962977

; GENERAL INFORMATION:

; APPLICANT: ASANO, Shinichiro

; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,

; FILE REFERENCE: Q68821

; CURRENT APPLICATION NUMBER: US/10/089,678

; PRIOR FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: JP 2000-236140

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: PCT/JP01/06660

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 3504

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

; FEATURE:

; NAME/KEY: exon

; LOCATION: (1)..(3501)

; OTHER INFORMATION:

US-10-089-678-2

Query Match 6.4%; Score 380.8; DB 3; Length 3504;

Best Local Similarity 55.4%; Pred. No. 2.7e-75;

Matches 881; Conservative 0; Mismatches 622; Indels 87; Gaps 4;

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QY 2221 ACACGCTGACGATCTGTTTACCAATTAACAAATAATTTACTAGATAGTGGTATT 2280
DB 1953 AGGAGGAGAGGTTTATGTAGATAAGTTTCGAACCTTATTCGGGTAAATGCAACATTTGAAGC 2012
QY 2281 GCTGTTTAAACAATAAGCGAAAGGTTGTGAGTCCCTATGTTTACAGTAGTAGCAAAAA 2340
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Db 2013 AGAAGAAGACCTAGATGTGGCAAGAAAGACGAGTAATAATGGCTGTGTTTACGAGTAAATAAAGA 2072

Qy 2341 TAGCTTAAAAATAGAAACACACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATG 2400

Db 2073 TGCCTTACAGACAGGTGAACGGATTATCAAGTGAATCAAGCGGCAAACTTAGTAGAATG 2132

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Db 2133 CCTATCCGATGATTTATACCCAAATGAAATAAGCAATGTTATGGGATGCGAGTGAAGAGGC 2192

Qy 2461 AAAACAACTTAGTCACTGCTGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGAT-- 2518

Db 2193 GAAACGACTTGTTCAGGACGTHAATCTTACTCCAGATACAGGCTTTTAATAGGATTAATGG 2252

Qy 2519 -----TGGACATTCGGTAATGATATTTATCATAGGATCCAATAATCCTATTTTTAA 2568

Db 2253 AGAAAAACGATGCGGGAAGTACGGGAATCGAGGTTGCGGAAGGAGATGTTCTGTTTAA 2312

Qy 2569 AGGAAAATTTTACAGATGGGTGGAGACAGACATATATGGNACTCTATTTCCAACTTA 2628

Db 2313 AGATCGTTCCGCTTCGTTTGACAAAGTCGAGAGAGATTGATACAGAAACATATCCAACTTA 2372

Qy 2629 TATCTCTCAAAAATAGATGAGTCTAAATTTAAACCATATACACGTTATCGAGTAAAGAG 2688

Db 2373 TCTCTATCAACAATAGATGAATCACTTTTAAACCATATACAGATATAAATCTAAAGG 2432

Qy 2689 GTTGTGGGAAGTAGTAAGATTGAAATTTAATGTTAAACAGTTTACGGGAAAGAAATTGA 2748

Db 2433 TTTTATAGGAAGTAGTCAAGATTTAGAGATTAATAATACGTCATCGGGCAATCAAT 2492

Qy 2749 TGCATCATGAATGTTCCAAATGATTTGGCTATATGCGAGCCTTAATCCTTTCATGTGGAGA 2808

Db 2493 CGTCAAAAATGTACCAAGATAATCTTGGCAGATGACTCCCTGTCAATTTCTTGTGGTG 2552

Qy 2809 TTATCGCTGTGAATCATGCTCTCAGTATGTGAGCCAAAGGTATCTTACCAACACATGS 2868

Db 2553 GATCGATCGCTGAGTACGACATGATGTAGACGGAAATTAGCACTCGAAACAAATGG 2612

Qy 2869 ATATGCTCCCGATATGATGCAATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCA 2928

Db 2613 AGAAAAATGGAATATGCTTCT----- 2634

Qy 2929 CGATCGTCACTCAATTTGATTTTTCATATTGACCCGAGAGTAGATACAAATACAATGT 2988

Db 2635 -GATTCCTTCCATGCAATTTCTTCTCCATATTGATACAGGTGAATAGATTGAATGAAATAC 2693

Qy 2989 AGGTATTGATGCTTATTAATAATTTCTAATCCAGATGGATACGCTACAGGAAATCT 3048

Db 2694 AGGAATTTGGTTCGTAATTTAATAATTCGACAAACAATGGATACGCAACACTAGGAATCT 2753

Qy 3049 AGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCACATGTGAAACAAAGA 3108

Db 2754 TGAATTTGGTAGAAGAGGGGCCATTGTCAAGGAAACATTAGAACGAGCAACAACAAGA 2813

Qy 3109 AAGAATATGGAACACACATGAGAGAAAACGTTGGGAAACACACAGCCCTATGATCC 3168

Db 2814 ACAACATGCAAGACAAATGCGAAGAAACGTTGGGCACTCAGAAAAGCATATTATGC 2873

Qy 3169 AGCAAAACAGGCTGTAGATGCAATTTTACAAATGAACAGAGTTTACACTATCATATTAC 3228

Db 2874 AGCAAGCAAGCCATTGATCGTTTATTCGAGATTTATCAAGACCAAAACTTAATTTCTGG 2933

Qy 3229 TTTAGA-----TCATATTCAAAACGCTGATCGATCGATCGATTCGATTCCTTATGATA 3282

Db 2934 TGTAGAAATGTCAGATATGTTGGCAGCCCAAAACCTTGTACAGTCCATTCCTTACGTATA 2993

Qy 3283 CCATATTTGGTTACCGATGCTCCAGTATGAACTATGATGATATCAAGAGTTAAACGC 3342

Db 2994 TAATGATGCGTTTACCAAGAAATCCCTGGAATGAATCATACGAGTTTACAGAGTTAAACAA 3053

Qy 3343 ACCTATCATGCAAGGTTTAATTTATGATGACGAAATGTATCAACAAATCGTGACTT 3402

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Qy 3403 TACAAGAGATTYACAGGATGCGACGCAACAGGAAATGCCGGGTACAACAAATGGATGG 3462

Db 3114 TCGAAATGGATTTAAGTGATTTGGAATGCAACATCAGATGTGAATGTGCAACAACTAAGCGA 3173

Qy 3463 AGCTTCAGTATTAGTTCCTATCAAAATGGAGCGCGGGGTATCTCAAACTTTGCATGCTCA 3522

Db 3174 TACATCTGTCTTGTTCATTTCCAACTGGAATTTCTCAAGTGTCAACAATTTTACAGTTCA 3233

Qy 3523 AGATCATCATGATATGTTTACGTGTGATTTGCCAAAAAAGAGACCTGGAAAAAGGTA 3582

Db 3234 ACCGAATATAGATATGTTTACGTGTACAGCGAGAAAAGAGGAGTAGGAGACGATA 3293

Qy 3583 TGTACAGATGATGGAATGTAATGGAAAGCAGGAAACACATTAAGTTTCACTTTTGGCAAGA 3642

Db 3294 TGTGATCATCCGTGATGTTGCGAATCAGACAGAAACACTCAATTTAATATATGTGATGA 3353

Qy 3643 AG-----GATATATGACAAAAACAGTAGAGGTATT 3672

Db 3354 TGATACAGGTGTTTTATCTGCTGATCAAACTAGCTATATCAGAAAAACAGTGGAAATTCAC 3413

Qy 3673 CCCAGAAAAGTTCGTGACGATTTGAAATAGGAGAAAACCGAAGGTACATTTTATATAGA 3732

Db 3414 TCCATCTACAGAGCAAGTTTGGATTGACATGATGAGACCGGAAGGTGATTTCACACATAGA 3473

Qy 3733 TAGCATCGAGTTGCTTTGTATGCAAGGATA 3762

Db 3474 AAGTGTAGAACTCGTGTTAGAAGAAGTA 3503

RESULT 4

US-10-089-678-3
; Sequence 3, Application US/10089678
; Patent No. 6962977
; GENERAL INFORMATION:

; APPLICANT: ASANO, Shinichi
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A
; FILE REFERENCE: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3690

; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-089-678-3

Query Match 6.4%; Score 380.8; DB 3; Length 3690;

Best Local Similarity 55.4%; Pred. No. 2.7e-75; Indels 87; Gaps 4;
Matches 881; Conservative 0; Mismatches 622

Qy 2221 ACGCGTGAAACGATCTGTTTACCAATTAAACCAAAATRAATTTACTAGAAATAGGTGGTATT 2280

Db 2139 AGGAGGAGAAGTTTATGTAGATAAGTTTCGAACCTTATTCGGTAAATGCAACATTTGAAAGC 2198

Qy 2281 GCTGTTTAACAATAAGCGAAAAAGGTTGTGAGTCTGTATTACAGTAGTAGTACGAAAAA 2340

Db 2199 AGAAGAAGACCTAGATGTGGCAAGAAAGACAGTAAATGSCCTTTGTTTACGAGTAAAAAAGA 2258

Qy 2341 TAGCTTAAAAATAGAAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCCTATAGAAATG 2400

Db 2259 TGCCTTACAGACAGTGTACCGATTATCAGTGTATCAGCGGCAAACTTAGTAGAATG 2318

Qy 2401 TATGTCAGATGAACAAAATCCTCAGGAAAAATAATGTTTATGGGATGAAATAAAACTGGC 2460

Db 2319 CCTATCCGATGATTTATACCCAAATGAAAAACGAATGTTTATGGGATGCAAGTGAAGAGGC 2378

US-07-915-203-1

Query Match 6.0%; Score 358; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 3.4e-70;
Matches 776; Conservative 0; Mismatches 530; Indels 60; Gaps 4;

QY 2297 GCGAAAGGGTGTGAGTCTCTATGTTTACAGTAGTACGAAATAATCGTTAAATAAGAA 2356
DB 2197 GCAAGAAAGCTGTGAATGGCTTGTGTTAC---GAATGAAAAAGATGCTTTACAGCAAGT 2253
QY 2357 ACACAGATATTGAAATAGATCAAGCGGCATTTCTATAGATGATGTGTCAGATGAACAA 2416
DB 2254 GTACCGATTTCAAGTCAATCAGCGGCAACCTTAATAGATGCTTATCCGATGAGTTA 2313
QY 2417 AATCTCTCAGGAAAAATAATGTTATGGGATGAAATAAACTGGCAAAACAACTTAGTCAG 2476
DB 2314 TACCCAAATGAAAAACGAATGTTATGGATGCAATGAAAGCGGAAACGACTGTTTCAG 2373
QY 2477 TCTCGTAATCTACTCAAATAATGGAGACTTTTCTGGGAATGAT-----TGGACA 2524
DB 2374 GCACGTAATCTACTCAAAGATACAGGCTTTAATAGGATTAATGGAGAAAAACGATGGAGC 2433
QY 2525 TTCGGTAATGATATTATCATAGGATCCAAATAATCCTATTTTTAAAGGAAAAATTTCTACAG 2584
DB 2434 GGAAGTACGGGAATCAGGTTGTGGAGGAGATGTTCTGTTTAAAGATCGTTCGCTTCGT 2493
QY 2585 ATGCGTGGAGCAGACACATATATGGAACCTCTATTTCCAACTTATATCTGTCAAAAAATA 2644
DB 2494 TTGACAAGTGGAGAGAGATTGATACAGAAACATATCCAAAGTATCTCTATCAACAAATA 2553
QY 2645 GATGAGTCTAAATTAATAAACCATATACAGTTATCGAGTAAGAGGGTTTGTGGGAATGAT 2704
DB 2554 GATGAATCGCTTTTAAACCATATACAGATATAAACTAAAAGGTTTATATAGGAATGAT 2613
QY 2705 AAGATTTCGAATTAATGTAACACGTTCAGGGAAGAAATTCGATCTCATGATGTT 2764
DB 2614 CAGATTGAGATTAATTAATATACGTTCAGGGAACAAATCAAACTGTCAAAATGTACCA 2673
QY 2765 CCAATGATTGTCCTATATGACAGCCTAATCTCTCATGTGGAGATTTATGCTGTGAATCA 2824
DB 2674 GATAATCTTGTCCAGATGTACGCCCTGTCAATTCCTTGTGTGGATCGATCGTCAAGT 2733
QY 2825 TCGTCTCAGTATGTAGCCAGAGGTATCTTACCAACACAGATGATGTCGCCGATATG 2884
DB 2734 GAACACAGTATGTAGACGCGAATTTAGCACTCGAAAAACAAATGGAGAAAAATGGAATATG 2793
QY 2885 TATGATGCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAACGATCGTCAATCATTT 2944
DB 2794 TCTTCT-----GATTCCTCATGCTTT 2814
QY 2945 GATTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATGCTTTA 3004
DB 2815 TCTTTCATATTGATACGGGTGAATAGATTTGAATGAAAAATACAGGAATTTGGATCGTA 2874
QY 3005 TTAATAATTTCTAATCCAGATGATACGCTACAGTAGGGAATCTAGAAGTCATTTGAAGAA 3064
DB 2875 TTTAAATTTCCGACAAACAAATGGAACCGCAACTAGGAAATTTGAAATTTGTAGAAGAG 2934
QY 3065 GGACCACTAACAGGTGAAGCATTTGGCAGCATGTGAAACAAAGGAAAAAGAAATGGAACAA 3124
DB 2935 GGGCCATTGTGAGGGGAAACATTAGAATGGGCCCAACACAGAACACAAATGGCAAGAC 2994
QY 3125 CACATGGAGAAAAACGTTTGGGAAACACAAACAGCCTTATGATCCAGCAAAACAGGCTGTA 3184
DB 2995 AAAATGGCAAGAAAAAGTGCAGCATCAGAAAAAACATATTTATGACGAAAGCAAGCAAT 3054
QY 3185 GATGCAATTTTACAATAGAACAGGATGTACACTATCATATTACTTTAGA-----TCAT 3238
DB 3055 GATCGTTTATTCGCAATTTATCAAGACCAAAAACTTTAATTCGTGTTAGAAATGTGAGAT 3114
QY 3239 ATTCAAAACGCTGATCGACTGGTACAGTCCCTATGTATATACCATTAATGTTGTTACCG 3298
DB 3115 TTGTTGGCAGCCCAAAACCTTTGTACAGTCCATTCCTTACGTATATATGATGCGTTACCG 3174

RESULT 6

US-08-272-887-1

; Sequence 1, Application US/08272887

; Patent No. 5747450

; GENERAL INFORMATION:

; APPLICANT: Ohba, Michio

; APPLICANT: Iwahana, Hidenori

; APPLICANT: Sato, Reichi

; APPLICANT: Suzuki, No. 5747450kazu

; APPLICANT: Ogiwara, Katsutoshi

; APPLICANT: Sakana, Kazunobu

; APPLICANT: Hori, Hidetaki

; APPLICANT: Asano, Shouji

; APPLICANT: Kawasugi, Tadaaki

; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/272,887

; FILING DATE: 08-JUL-1994

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/915,203

; FILING DATE: 23-JUL-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: M/K 301

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3797 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

QY 3299 AATGCTCCAGGTATGAACCTATGATGTATCAAGATTAAACGACGTATCATGCAAGGT 3358
DB 3175 GAAATCCCTGGAACTGAACCTATACGAGTTTTACAGAGTTTAAACAAATAGACTCCCAACAGCA 3234
QY 3359 TATAATTTATATGATGACGAAATGTCTATAACAAATGGTGACTTTTACACAGGATTCAG 3418
DB 3235 TGGAAATTTGATGATCTTCAAAACGCTATACCAAAATGGAGATTTTTCGAAATGGATTAAGT 3294
QY 3419 GGATGGCAGCGCAACAGGAAATGCCCGGTACACAAATGGATGGAGCTTCAGTATTAGTT 3478
DB 3295 AATTGGAATGCAACATCAGATGAATGTGCAACAACTAAGCGATACATCTGCTCTGTC 3354
QY 3479 CTATCAAAATGGAGCGCGGGGTATCTCAAACTTTGCAATCTCAAGATCATCATGATAT 3538
DB 3355 ATTCCAAACTGGAATTTCTCAAGTGTCAACAAATTTACAGTTCAACCGAATTTATAGATAT 3414
QY 3539 GTGTTACGTGTGATTTGCCAAAAAGAGGACCTCGAAAAAGGTATGTAAACGATGATGAT 3598
DB 3415 GTGTTACGTGTCAACGCGAGAAAAAGAGGAGTAGGAGACGGATATGTGATCATCCGTGAT 3474
QY 3599 TGTAAATGGAAGCAGCAACACTTAAAGTTTCACTTCTTTCGAAAGAAG 3644
DB 3475 GGTGCAATCAGACAGAAACACTCACATTTAATATATGTGATGATG 3520

US-08-272-887-1

; Sequence 1, Application US/08272887

; Patent No. 5747450

; GENERAL INFORMATION:

; APPLICANT: Ohba, Michio

; APPLICANT: Iwahana, Hidenori

; APPLICANT: Sato, Reichi

; APPLICANT: Suzuki, No. 5747450kazu

; APPLICANT: Ogiwara, Katsutoshi

; APPLICANT: Sakana, Kazunobu

; APPLICANT: Hori, Hidetaki

; APPLICANT: Asano, Shouji

; APPLICANT: Kawasugi, Tadaaki

; TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/272,887

; FILING DATE: 08-JUL-1994

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/915,203

; FILING DATE: 23-JUL-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: M/K 301

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3797 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: japonensis
INDIVIDUAL ISOLATE: Buibui
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3636
US-08-272-887-1

Query Match 6.0%; Score 358; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 3.4e-70;
Matches 776; Conservative 0; Mismatches 530; Indels 60; Gaps 4;

QY 2297 GCGAAAAAGGTGTGAGTCTCTATGTTTACAAAGTAGTACGAAAAATACGTTTAAAAATAGAA 2356
DB 2197 GCAAGAAAGCTGTGAATGGCTTGTTTTAC---GAATGAAAAAGATGCTTTACAGCAAGT 2253
QY 2357 ACACAGATTTATGAATAGATCAAGCGGCCATTTCTATAGAATGTATGTGATGATGAACAA 2416
DB 2254 GTAACGATTTATCAAGTCAATCAAGCGGCAACTTAATAGATGCCCTATCCGATGAGTTA 2313
QY 2417 AATCCTCAGAAAAAATAATGTTATGGATGAATAAACTGCGCAAAACAACTTAGTCAG 2476
DB 2314 TACCCAAATGAAAAACGAATGTTATGGATGCGATGAAAGAGGCGAAACGACTTGTTCAG 2373
QY 2477 TCTCGTAATCTCTCCAAATGAGACTTTTCTGGGATGAT-----TGACA 2524
DB 2374 GCACGTAATCTCTCCAAAGATACAGGCTTTAATAGGATTAATGGAGAAAAACGGATGGACG 2433
QY 2525 TTCCGTAATGATATTATCATAGGATCCAAATAATCTTATTTTAAAGGAAAAATTTCTACAG 2584
DB 2434 GGAAGTACGGATCGAGTGTGGAGGAGATGTTCTGTTTAAAGATCGTTCGCTCGT 2493
QY 2585 ATCGGTGGACGACGACATATATGGAATCTATTTCCAACTTATCTGTCAAAAAATA 2644
DB 2494 TTGACAAAGTCGAGAGAGATTTGATACAGAAACATATCCAACTATCTCTATCAACAAATA 2553
QY 2645 GATGAGTCTAAATTAACCATATACAGTTATCGAGTAGAGAGGTTTGTGGAAAGTAGT 2704
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QY 2705 AAAGATTGAAATTAATGTTAAACAGCTTACGGGAAAGAAATTCATGCTATCATGATGTT 2764
DB 2614 CAGATTTAGAGATTAATTAATACGTATCGCGGCAATCAAACTGTCAAAAATGTACCA 2673
QY 2765 CCAATGATTTGCGCTTATATGCGAGCTTAATCTTCATGTGGAGATTTATCGCTGTGAATCA 2824
DB 2674 GATAATCTCTGCCAGATGTACGCCCTGTCAATTTCTGTGGTGGAGTCGATCGCTCGAGT 2733
QY 2825 TCGTCTCAGTATGTAGCCNAGGATCTCTACACCAACAGATGATGATCGTCCGATATG 2884
DB 2734 GAACACAGTATGTAGACCGGAATTTAGCACTCGAAACCAATGGAGAAAAATGGAATATG 2793
QY 2885 TATGATGCGCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAACGATCGTCATCATTT 2944
DB 2794 TCTTCT-----GATTCCTGATGATTT 2814
QY 2945 GATTTTCATATTCACACCGAGAGTAGATACAAATACAAATAGGTATGTATGTCTTA 3004
DB 2815 TCTTTCATATTCATACCGGTGAATAGATTTGAATGAAAAATACAGGAATTTGGATCGTA 2874
QY 3005 TTAATAATTTCTAATCCAGATGATACGCTACAGTAGGGAATCTAGAAGTCATTTGAAGAA 3064
DB 2875 TTTAAATTTCCGACAAACAAATGGAACGCAACTAGGAATTTGAATTTGTAGAAAGT 2934
QY 3065 GGACCACTAACGCTGAAGCATTTGGACATGTGAAACAAAGGAAAAAGAAATGGAACAA 3124
DB 2935 GGGCCATTTGCGGGGAAACATTTAGATTTGGGCCAACACACAGNACAAATGGCAAGAC 2994
QY 3125 CACATGGAGAAAAACGTTGGGAAACACCAACAGCCTATGATCCAGCAAAACAGGCTGTA 3184

DB 2995 AAAATGCAAGAAAAAGTCAGCATCAGAAAAACATATTTATGTCAGCAAGCAAGCCATT 3054
QY 3185 GATGCAATTTATTAACAATGAACAAGAGTTACACTATCATATTTACTTTAGA-----TCAT 3238
DB 3055 GATCGTTTATTCGAGATTTATCAAGACCAAAAACTTAATTTCTGGTGTAGAAATGTCCAGAT 3114
QY 3239 ATTCAAAAGCGCTGATCGACTGGTACAGTATCCCTATGTATATACCATTAATTTGTTTACCG 3298
DB 3115 TTGTTGGCAGCCCAAAACCTTGTACAGTCCATTTCTGATATATATGATGCTTTTACCG 3174
QY 3299 AATGCTCCAGGTATGAATCATGATGATATCAAGAGTTTAAACGACGATCATATGCAAGGT 3358
DB 3175 GAAATCCCTGGAATGAATATACGAGTTTACAGAGTTTAAACAAATAGACTCCCAACAGCA 3234
QY 3359 TATTAATTTATGATGACGAAATGTATCAACAAATGGTGACTTTTACACAGAGATTTACAG 3418
DB 3235 TGAATTTGTATGATCTTCAAAACGCTATATCAAAATGGAGATTTTCCGAAATGGATTAAGT 3294
QY 3419 GGATGCGACGCAACGAAATGCCGGGTACAAATGGATGGAGCTTCAGTTCAGTATTAGTT 3478
DB 3295 AATGGAATGCAACATCATGATGTAATGTGCAACAACTAAGCGATACATCTGCTTGTGTC 3354
QY 3479 CTATCAAAATGGAGCGCGGGGTATCTCAAACTTGCATGCTCAAGATCATCATGATAT 3538
DB 3355 ATTCCAACTGGAATTTCTCAAGTGTCAACAAATTTACAGTTTCAACCGAATTTATAGATAT 3414
QY 3539 GTGTTACGTGTGATTTCCCAAAAAAGAGAGACCTGGAAGGGTATGTAAAGATGATGGAT 3598
DB 3415 GTGTTACGTGTACAGCGAGAAAGAGGAGTAGGAGCGGATATGTGATCATCCGTGAT 3474
QY 3599 TGTAAATGGAAAGCAGGAAAACTTAAAGTTTCACTTCTTTCGAAAGAG 3644
DB 3475 GGTGCAAAATCAGACAGAAACATCTCATTATATATGATGATGATG 3520

RESULT 7

US-08-789-449-1
; Sequence 1, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwahana, Hidenori
; APPLICANT: Sato, Reichi
; APPLICANT: Suzuki, No. 5824878ukazu
; APPLICANT: Ogiwara, Kateutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasugi, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: japonensis
; INDIVIDUAL ISOLATE: Buihui
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3636
; US-08-789-449-1

Query Match      6.0%; Score 358; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 3.4e-70;
Matches 776; Conservative 0; Mismatches 530; Indels 60; Gaps 4;

QY 2297 GCGAAAGGTTGTGAGTCTCTATGTTTACAAAGTAGTACGAAAGGTTTCTATAGATGTATGTCAGATGACAA 2356
DB 2197 GCAAGAGAGCTGTGAAGTGGCTTGTGTTTAC--GAATGAAAGAGATGCCCTTACAGACAAGT 2253
QY 2357 ACGACAGATATCAAAATAGATCAAGCGGCCATTTCTATAGATGTATGTCAGATGACAA 2416
DB 2254 GTAACGGATTTTCAAGTCAATCAAGCGGCAAACTTAATAGATGCGCTATCCGATGAGTTA 2313
QY 2417 AATCCTCAGGAAAGGTTATGTTATGGATGAAATAAACTGSCAAAGCAACTTACTGTAG 2476
DB 2314 TACCCAAATGAAAGCAATGTTATGGATGCACTGAAAGCGGAAACGACTTGTTCAG 2373
QY 2477 TCTCGTAATCTACTCCAAATGGAGACTTTTCTGGGAATGAT-----TGGACA 2524
DB 2374 GCACGTAACTTACTCCAGATACAGGCTTTAATAGGATTAATGGAGAAACGGATGGACG 2433
QY 2525 TTCGGTAATGATATTATCATAGATCCAAATATCCTATTTTAAAGGAAATTTCTACAG 2584
DB 2434 GGAAGTACGGGAATCAGGTTGTGSAAGGAGATGTTCTGTTTAAAGATCGTTTCGCTTCT 2493
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DB 2494 TTGACAAGTGGAGAGAGATTGATACAGAAACATATCCAACTGTTCTCTATCAACAAATA 2553
QY 2645 GATGAGTCTAAATTTAAACCATATACACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGT 2704
DB 2554 GATGAATCGCTTTTAAACCATATACAGATATAAACTAAAGGTTTATAGGAAGTAGT 2613
QY 2705 AAGATTTCGAATTAATGTTACACGCTTACCGGAAAGAAATTCATCTATCATGAATGTT 2764
DB 2614 CAAGATTTAGAGATTAAATTAATACGTCTATCGGGCAAAATCAAAATCGTCAAAAATGTACCA 2673
QY 2765 CCAAAATGATTGGCTTATATGACGCTTAATCCTTTCATGCGAGATTATCGCTGTGAATCA 2824
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QY 2825 TCGTCTCAGTATGTGAGCCAAAGGGTATCCCTACACCAACAGATGGATATGCTCCCGATATG 2884
DB 2734 GAACACAGATGTAGACGGGAATTTAGCACTCGAAGCAATGGAGAAAAATGGAATATG 2793
QY 2885 TATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTGCACATCGTCAATCCATTT 2944
DB 2794 TCTTCT-----GATTCCTCCATCGATTT 2814
QY 2945 GATTTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATGCTTAA 3004
DB 2815 TCTTTCATATTGATACGGGTGAATAGATTGTAATGAAATACAGGAATTTGGATCGTA 2874

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RESULT 8

US-07-876-280-29

; Sequence 29, Application US/07876280

; Patent No. 5262158

; GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.

; APPLICANT: Cannon, Raymond J.C.

; APPLICANT: Bagley, Angela L.

; TITLE OF INVENTION: NO. 5262158el Bacillus thuringiensis Isolates for

; NUMBER OF SEQUENCES: 30

; TITLE OF INVENTION: Controlling Acarides

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/876,280

; FILING DATE: 19920430

; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: E. coli NM522 (pMYC2320) NRRL B-18769
US-07-876-280-29

Query Match . 5.3%; Score 314.6; DB 2; Length 3471;
Best Local Similarity 55.7%; Pred. No. 1.7e-60;
Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps 8;
QY 2292 AATAAGCGAAAGGTTGTGAGTCCTATGTTTACAGTAGTAGCGAAATAACGTTAAAAA 2351
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QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTCTTATAGAAATPATGTCTAGATG 2411
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QY 2412 AACAAATCTCAGGAAAAAATATGTATGGATGAAATPAAACTGGCAAAACAACCTTA 2471
DB 2132 ATTTATATCCAAATGAAACAGATTGTTATTTGATCGGTGAGAGAGGCAAAACGCTCA 2191
QY 2472 GTCAAGTCTGTATCTACTCCAAATGGAGACTTTTCTGGG-----AATGATT 2519
DB 2192 GTGGGCGACGTAATCTACTCAAGATCCAGATTCCAAAGAGATPAAACGGAGAAATGGAT 2251
QY 2520 GGACATTCGGTATGATATTATCATAGGATCCCAATATCTATTTTAAAGGAAATTTTC 2579
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DB 2312 TACGCCTACCAGGTGCACGAGAAATTTGATACGGAACGATATCCACGATATCTGTATCAA 2371
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DB 2372 AAGTAGAGGAAGGTGTATTAAACCCATACACAAAGATATAGACTGAGAGGGTTTGTGGGAA 2431
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DB 2432 GTAGTCAGGATTAGAAATTTATACGATACGTCAC---CAAACGAATCGAATTTGTAAGA 2488
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DB 2489 ATGTACCAGATGATTATTGGCCA-----GATGTATCTCTGTGA 2526
QY 2820 AATCATGCTCTAGTATGTGAGCAAGGGTATCTTACCAACAGATGGATATGCTCCCG 2879
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DB 2675 TTGGATTTAAGATTACGGACCCAGAGGGATACGCAACACTTTGGAATTTAGTTCG 2734
QY 3060 AAGAAGGACCACCTAAACAGGTGAAGCAATTCGCACATGTGAACAAAGAAAGAAAGAAATGGA 3119
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DB 3395 ATCAAAATGTGGATTGAAATTAAGTGAACAGAGGATACGTTCTATATAGAAAGTGTAGNAT 3454
QY 3744 TGCTT 3748
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RESULT 9

US-07-812-180A-1
; Sequence 1, Application US/07812180A
; Patent No. 536892
; GENERAL INFORMATION:
; APPLICANT: .Foncerrada, Luis R
; APPLICANT: Payne, Jewel M
; APPLICANT: Sick, August J
; TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
; TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding a
; TITLE OF INVENTION: Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```
/ ADDRESS: Roman Saliwanchik
/ STREET: 2421 N.W. 41st Street, Ste A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/812,180A
/ FILING DATE: 19920102
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, Roman
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3471 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus thuringiensis
/ STRAIN: kumamotoensis
/ INDIVIDUAL ISOLATE: P850C
/ IMMEDIATE SOURCE:
/ LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
/ CLONE: 50C
/
/ US-07-812-180A-1
/
/ Query Match 5.3%; Score 314.6; DB 2; Length 3471;
/ Best Local Similarity 55.7%; Pred. No. 1.7e-60;
/ Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps 8;
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/ QY 2292 AATAAGCGAAAAAGTTGTGAGTCTATGTTTCAAGTAGTAGTACGAAAAATACGTTAAAAA 2351
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/ QY 2352 TAGAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATAGAAATGTATCTCAGATG 2411
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/ QY 2412 AACAAAATCCTCAGGAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACAACTTAA 2471
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/ QY 2472 GTCAGTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGG-----AATGATT 2519
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/ QY 3000 TCTTATTTAAAAATTTCTAATCCAGATGGATAGCTACAGTAGGGGAATCTAGAAATGATG 3059
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/ QY 3060 AAGAAGGACCACTAACAGGTGAAGCATTTGGGCACATGTGAACAAAGAAAGAAATGGA 3119
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/ QY 3180 CTGTAGATGCATTTATTACAAATGAAACAGAGTTACACTATCATATTTACTTTAGA----- 3234
/ DB 2855 CGGTAGATCGTTTATATCCGATTTATCAGGATCAACAACTGAATCCTGATGTAGAGATTA 2914
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/ QY 3235 -TCATATTCAAAACGCTGATCGACTGTGACAGTCCCTTATCTATGTATACCAATATGTTGT 3293
/ DB 2915 CAGATCTTACTGCGGCTCAAGATCTGATACAGTCCCTTCTTACGTATATAACGAATGT 2974
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/ QY 3294 TACCGAATGCTCCAGGTATGAACCTATGATGTATATCAAGAGTTAAACGCAAGTATCATGC 3353
/ DB 2975 TCCAGAAATACACAGGGATGAACCTATACGAAGTTTACAGAATTAACAGATCGACTCCAAC 3034
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/ QY 3354 AAGGTTTAAATTTATATGATGCAAGAAATGTATACAAATGGTGCATTTTACACAGGAT 3413
/ DB 3035 AAGCGTGGAAATTTGTATGATCAGCGAAATGCCATACCAATGGTGTGATTTTCGAAATGGGT 3094
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/ QY 3414 TACAGGGATGGCAGCAACAGGAAATGCCGGGTACAAACAAATGGATGGAGCTTCAGTAT 3473
/ DB 3095 TAAGTAAATTGGNAATCGAACGCTGGCGGTAGAGTACAAACAAATCAATCATATCTGTCC 3154
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/ QY 3474 TAGTTCTATCAAAATGGAGCGGGGTATCTCAAAACTTGCATCTCAAGATCATCATG 3533
/ DB 3155 TTGTGATTTCCAACTGGGATGAAACAAAGTTTCAACACAGTTTACAGTTCAACCGGAATCAA 3214
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/ QY 3534 GATATGTGTAGTGTGATTTGCCAAAAAAGAGGACCTTGGAAAAAGGTTATGTAAACGATGA 3593
/ DB 3215 GATATGTATTACAGTTTACTGCAAGAAAGAGGGGTAGGAAATGGATATGTAAGTATTC 3274
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/ QY 3594 TCGATTGTAAATGGAAGCAGGAAACACTTAAAGTTCACTTCTTTCGCG----- 3638
/ DB 3275 GTGATGGTGGAAATCAATCAGAAACGCTTACTTTTGTAGCAAGCGATTTATGATACAAATG 3334
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/ QY 3639 -----AAGAAGGATATATGACAAAAACAGTAGAGGATTTCCAGAAAGTG 3683
/ DB 3335 GTGTGTATAATGACCAACCGCTATATCACAACAAACAGTGACATTCATCCCGTATACAG 3394
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/ QY 3684 ATCGGTGACGATTTGAAATAGAGAAACCGAGGTACATTTTATATAGATACATCGAGT 3743
/ DB 3395 ATCAAAATGGGATTGAAATTAAGTGAACAGAGGTCGTTCTATATAGAAAGTGTAGAAT 3454
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/ QY 3744 TCGTT 3748
/ DB 3455 TGAAT 3459
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RESULT 10
US-08-315-468-1
; Sequence 1, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
; APPLICANT: Michaels, Tracy Ellis
; APPLICANT: Fonceerrada, Luis
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Process for Controlling Scarab Pests
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,468
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,941
; FILING DATE: 01 FEB 1993
; APPLICATION NUMBER: 07/828,430
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/808,316
; FILING DATE: 16-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA73.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: kumamotoensis
; INDIVIDUAL ISOLATE: PS50C
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF LUIS
; CLONE: 50C(a)
US-08-315-468-1

Query Match 5.3%; Score 314.6; DB 2; Length 3471;
Best Local Similarity 55.7%; Pred. No. 1.7e-60;
Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps 8;
QY 2292 AATAAGCGAAAAGTTGTGAGTCTTGTACAGTAGTACGAAAATACGTTAAAAA 2351
DB 2015 AACGGCGAAGAAGCAGTGAATGCTTTTAC---GAATACAAAAGATGGCTTACGAC 2071
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTCTCTAGAAATGTATGTCAGATG 2411

DB 2072 CAGGTCTAACGGATTATGAAGTAAATCAAGCGGCAAACTTAGTGAATGCTATCGGATG 2131
QY 2412 AACAAAATCTCAGGAAAAAATAATGTTATGGGATGAATAAATACTGGCAAAACAACTTA 2471
DB 2132 ATTTATATCCAAATGA AAAACGATTGTTATTTGATCGGTGAGAGAGGCAAAACGCGCTCA 2191
QY 2472 GTCAGTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGG-----AATGATT 2519
DB 2192 GTGGGGCAGTAACTTACTACAAGATCCAGATTTCAGAGAGATAAACGGAGAAAATGGAT 2251
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QY 3000 TCTTTATTAATAATTTCTTAATCCAGATGGATAGCTACAGTACAGTGGGAATCTAGAGATCAT 3059
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DB 3095 TAAGTAATTTGGAATGCACCGCTGGCGTAGAAGTACAAACAATCAATCATATCATCTGTCTC 3154

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Db 888 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAAATGGTTTGTACATCGTAGTGTCT 947
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Db 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAATAGA-----GCTAAATTTCTCAGATTTAGA 1001
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QY 1577 TAATGTTGTAGAGGACCTCTCATAGATTATCAAAATCGGCATGTGTTGTATATGAA 1636
Db 1337 CAACTGGGATAGATAACCC-----TAGAGTTCAAAATATTAACACTATTTTACCTGGAGA 1391
QY 1637 CTCACAGTTAAACGTATATGTTGGACACATACAAAGTTTAAACGTGAAATATAANTGA 1696
Db 1392 AAATTCAGATATCCCACTCCAGAGACTATATCTCATATATTAAGCACAAATAAATTT 1451
QY 1697 AGCAATCAAAATPACAAATACCGCGGTGAAGATTTATACCTTCAAAATTTATCTGC 1756
Db 1452 AACAGGAGGACTTAGCAAGTAGCATCTAATCCCGTTCATCTTTAGTAATGATGTTGGTTG 1511
QY 1757 TAATGCTTATACCTATGTAATAAAGCACTCAT- CAGGTGGGNTTTAATCCGTTTT 1814
Db 1512 GACATAAAGTCTGGCTCGTAACAAATACCAATTAATCCAGATAGAAATACAGATACC 1571
QY 1815 TTAAGAACAAAATCAGAGTATAACGAGTTTATGCAAGGTGGCGGAATTAGATTGATTT 1874
Db 1572 TTTAGTGAAGGATTTAGAGTTTGGGGGGCACTCTGTCAATTTACAGGACCAGATTTAC 1631
QY 1875 AATAACAAACTCGAGACAAAGTTACCGTAITTCGTTTTCGTTTATGCTGCAGATAAAGCT 1934
Db 1632 AGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTTGTATCTCTACAAGTCAATAT 1691
QY 1935 GCTTTCTTTAGTGATATCTTTATCCAGGAGTTGGGGTTCAATCGTTTGTATCGCTT 1994
Db 1692 TAATTCACCAAT-TACCCAAAGATACCGTTTAAGATTTTCGTTACGTTCCAGTAGGATG 1750
QY 1995 GAAAAATCTTACTCTGGAATTTAGCAGATTTAAAAATATAGTGAATTTAAATTCGCTGAA 2054
Db 1751 CACGAGTTATAGTATTAAACAGGACGGCATCCACAGGAGTGGGAGGCCAAGTTAGTGTA 1810
QY 2055 ATTATCACACCTCCATTAACCTAGTTCCAAACATTCAGATGATGTGAGATGCAAGCGAAT 2114
Db 1811 AT-----ATGCTCTCTCAGAAAACCTATGGAATAGGGAGAACTTTAAATCT 1857
QY 2115 AGTTTTCAATCAGATGTAACGTTGTTCTCGACAAAAATGGAATTTCTCCCAAGTAATACA 2174

Db 1858 AG--AACATTTAGATATACCGATTTTAGTAATCTCTTTTTCATTTTAGAGCTAATCCAGATA 1915
QY 2175 ACAACTTTTAGAATATAGGGAGAACGGACCTTAGAAAAAACAAGAACCGGTGACCAT 2234
Db 1916 TAAATGGGATAGTGAAACAACCTCTATTGTTGGTGCAGGTTCTATTAGTAGCGGTGAACTTT 1975
QY 2235 CTGTTTACCAATTTAAAAACAAATAATTTACTAGTAATAGGTGGTATGCTGTTTAA--CA 2291
Db 1976 ATATAGATAAAATTTGAAATTTATTTAGCAGATGCAACATTTTGAACAGAAATCTGATTTAG 2035
QY 2292 AATRAGCGAAAGGTTGTGAGTCTCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA 2351
Db 2036 AAGAGCACAAAGGCGGTGAATGCCCTGTTTACTTCTTCCNATCAATTCGGGTTTAAAAA 2095
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGGGGCCATTTCTATAGAAATGTATGTCCAGATG 2411
Db 2096 CCGATGTGACCGATTATCATATTGATCAAGTATCCAAATTTAGTGGATTTTATCCAGATG 2155
QY 2412 AACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATMAAACTGGCAAAAACAATTA 2471
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QY 2472 GTCACTCTCTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGATTTGGACATTCGTA 2531
Db 2216 GTGATGAGCGGAAATTTACTTCAAGATCCAACTTCAGAGGGATCAATAGACNACCAGACC 2275
QY 2532 ATGATATTATCATAGGATCCAATAATCTCTATTTTAAAAAGGAAATTTTCTACAGATGCGTG 2591
Db 2276 GTGGCTGGAGGAGTAGTACAGATATTACCATCCAAGGAGGAGTACCGTATTTCAAAGAGA 2335
QY 2592 GAGCAGGAGACATATATGGAATCT-----ATTTCCAACTTATATCTGTCAAAAA 2642
Db 2336 ATTACGTCACACTACCGGTACCGTTGATGAGTGTCTATCCAACTTATTTATATCAGAAA 2395
QY 2643 TAGATGAGTCTAAATTTAAAAACCATATACACGTTATCGAGTAGAGGTTTGTGGCAAGTA 2702
Db 2396 TAGATGAGTCGAAATTTAAAGCTTATACCGGTTATGAAATTAAGGGGTATATTCGAAGATA 2455
QY 2703 GTAAAGATTTGAAATTAATGTTGTAACAAGTTAGGGGAAAGAAATTTGATGCTATCATGATG 2762
Db 2456 GTCAAGACTTAGAAATCTATTGATCCGTAC--AATGCAAAAACAGAAATAGTAAATG 2512
QY 2763 TTCCAAATGATTTGGCCTTATATGACGCTTAATCTTCAATGTGGAGATTTATCGCTGTGAT 2822
Db 2513 TGCCAGCAGCAGGTTTCTTATGGCGCTTTTCAGCCCAAGTCCAAATCGGAAAGATGGAG 2572
QY 2823 CATCGTCTCAGTATGTGAGCCAAAGGTTATCTTACACCAACAGATGGATATGCTCCCGATA 2882
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QY 2883 TGTATGCAATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCCAGATCGTCAATCAT 2942
Db 2615 TAGATTGTTCTTCGACAGACGGGAAAAA-----TGTGCACATCATTTCCCATCAT 2665
QY 2943 TTGATTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGATGATTTGATGTCT 3002
Db 2666 TCACCTTGGATTTGATGTTGGATGTACAGACTTAAATGAGGACTTAGGATGATGGGTGA 2725
QY 3003 TATTTAAAAATTTCTAATCCAGATGATAGCTTACAGTAGTAGGGAATCTTAGAAGTCAATTGAAG 3062
Db 2726 TATTCAAGNTTAAGACGCAAGATGCCATGCAAGACTAGGGNATCTAGAGTTTCTCGAAG 2785
QY 3063 AAGGACCACTTAAACGGTGAAGCATTTGGCACAATGTGAAAAACAAAGAAAAAGAAATGGAAC 3122
Db 2786 AGAAACCAATTTATTAGGGGAAGCACCTAGCTCGTGTGAAAAAGAGCGGAGAAAGTGGAGAG 2845
QY 3123 AACACATGGAGAAAAAAGCTTGGGAAAACACAAAGCCCTATGATCCAGCAAAACAGGCTG 3182
Db 2846 ACACACGAGAGAAATCTGAGTTTGGAAAAAATAATTTGTTTATAAAGAGGAAAAAGATCTG 2905
QY 3183 TAGATGCAATTTTAAATAATGAAACAAG-----GTTACACTTATCATATTTACTTTAGATC 3236
Db 2906 TAGATGCTTTATTGTTAAACTCTCAATATGATAGATTACAAGTGGATACGACATCCGCA 2965

QY 3237 ATATTCAAACGCTGATCGACTGCTAGTCGATTCCTATGTATATACCATTAATTGGTTAC 3296
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Db 2966 TGATTCATCGGCAGATAAAGCGCTTCATAGAAATCCGGGAAGCATATCTGCCAGAGTTGT 3025
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QY 3297 CGAATGCTCCAGGTATGAATCATGATATATCAAGAGTTTAAACGACGCTATCATGCAAG 3356
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Db 3026 CTGTGATTCAGAGTGTCAATCGGCCATTTTCGAAGAATTAGAGGGACGTATTTTACAG 3085
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QY 3357 GTTATATTTATATGATGACGAAATGTCATACAAATGTGTGACTTTACACAGGATTAC 3416
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Db 3086 CGTATTCCTTATATGATGCGAGAAATGTCAATTAATAATGCGATTTCAATAATGGCTTAT 3145
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QY 3417 AGGATGCGACGCAACAGGAAATCGCGCGGTACAAA---CAATGGATGGAGCTTCAGTAT 3473
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Db 3146 TATGCTGGAACGTGAAGGTCATGTAGATGTAGAGAGCAAAACACCCGTTCCGTCC 3205
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QY 3474 TAGTTCTATCAAAATGGAGCGCGGGGTATCTCAAAATTTGCAATGCTCAAGATCATCATG 3533
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Db 3206 TTGTTATCCAGAAATGGAGGACGAAGTGTCAAAAGAGGTTCTGTCTGTCCAGGTCGTG 3265
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QY 3534 GATATGTTTACCTGTGATTTGCCAAAAGAGGACCTGAAAAGGATGTAAACGATGA 3593
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Db 3266 GCTATATCTTCGTGTCAACGATATTAAGAGGGATATCGAGAGGGCTGCGTAACGATCC 3325
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QY 3594 TGGATTGTAATGGAAGCAGAAACACTTAAAGTTTCACTTCTTCCGAAGAG 3644
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Db 3326 ATGATCGAGACNATACAGACGAACTGAAATTCAGCAACTGTGTAGAAG 3376
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RESULT 13

US-09-668-650-11
; Sequence 11, Application US/09668650
; Patent No. 6780408
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6780408artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,650
; FILING DATE: 22-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3726
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-09-668-650-11

Query Match 5.2%; Score 308.2; DB 3; Length 3726;
Best Local Similarity 48.0%; Pred. No. 4.6e-59;
Matches 1607; Conservative 0; Mismatches 1588; Indels 156; Gaps 19;

QY 323 AATTTGGGAATCAGTCCGAAACGATACCAAGTATTTGGGATATAATCTTTATAGAGTTTGTGAT 382
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Db 153 AATAGCGGATGCAGCAAAAGACGAGTATCTATTGGGACACCATAGTCTCTCTTATCAC 212
| | | | |
QY 383 AGAACCTAGTTTGGGTGGGAATTAATACACTATTAT-----CAATATAGGAAAACTAAT 436
| | | | |
Db 213 AGCACCTTCTCTTACTGCGATTAATTTCAATAGTATATGACCTTTATAGGTAAGTACTAGG 272
| | | | |
QY 437 TCCGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGCTGATTTTATATCTATATATTCG 496
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Db 273 AGTAGTAGTGGAACAATCCATATCAGATTTGTCTATATGTGACTTATATCTATATTATGA 332
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QY 497 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTGTGATGCGATTGCGAGATTTTTCGCGTAAATTTGAA 556
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Db 333 TTTACGGGTAAAGTCAGAGTGTGTTTAAATGATGGGATGCGAGATTTTAAATGGTCTGTACT 392
| | | | |
QY 557 AAATATAGAGAGTATTTATCTTTCTTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 616
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Db 393 CTTATACAGGAACTATTTAGAGGCTCTGGATAGTGGAAATAGAAATCCTAAATCTCTGCTTC 452
| | | | |
QY 617 TCAAAAGACAAATTAATCTCGATATCGGACAAATAGTTTATTTTAAACTTTTCAGAAAG 676
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Db 453 TGCTGAAGAACTCCGTAATCTGTTTGTAGAAATCGCGACTCAGAAATTTGTATAGAAATTTAAC 512
| | | | |
QY 677 AGATTTCAATGAAATCTTAGGAGGGTCAATGTCAGAAACAAATGCTCAAGTATGTTTATT 736
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Db 513 CCGAGGGTCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCAAATATATTATT 572
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QY 737 ACTTACTTTTGCACAAAGTCGCAATGTGCGAGTTTATCTATTAAAGGATGCGAGTTCAATA 796
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Db 573 ACCTTCTTTTGGAGCGCTGCAATTTTCCATTTATTTACTACTAAGGGATGCTACTAGATA 632
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QY 797 TAAAGCACAAATGTTTCCCAATTTTNGATGCGAGAGATGTAAGATCGGAATTAATATCACC 856
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Db 633 TGGCACTAATTTGGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
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QY 857 TAAACAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTTAAATAATGCAAAACGGCAGA 916
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Db 693 AGAGCTTATT-----GAACT 707
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QY 917 GTATACCAATTTATGTTTATATGTTATGTTATGTTATGTTTAAATCAGATATAAAGAGGGGG 976
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Db 708 ATATACGTATTTATGCTACATTTGTTATTAATGCGAGTTTCAACGAACTAAGACAAACGAGG 767
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QY 977 GACAGTCTGACACTTGGTCCAAATTTAATAAATTTGTTAGAGAAATGACGTTGGCGGT 1036
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Db 768 CACTAGTGTCTACAGCTTGGTTAGAAATTTCAATAGATATCGTAGAGAGATGACATTTGATGT 827
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QY 1097 TGTAGAGTTGACTAGGAAATTTATACAGATCAGTGGGATATTCATCGGAACTTTATAG 1156
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Db 888 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAAATGCTTTGTTGTACATCGTAGTAGTCT 947
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QY 1157 TTGTTTACCGAATTCGCCTAATCTTTTAAATGGGTTAGAGGCTATGNAACACGGGACC 1216
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QY 1217 TGGTTTAGTTACTTGGCTTAGCAAAATAGGTATATATATATGATGATGTTTCCAGATATTT 1276
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Db 1002 AATGCAATACCTAATCCTAG-ACCGTCTTGGTTTTAAATAATATGATTTATATCTACTG 1060
Qy 1277 TGC CGGCTGGTAGGAACCTGTCATTTATGAAGACTACACAAAGGGTAACGGTATTTTCA 1336
Db 1061 GTTCACCTTACATTTGCCGTTAGCCCAAGTACTGATAGAGCGAGGGTATGG----TATGG 1115
Qy 1337 ACGTATGCTGGAACCTACAGGTAATGATCTACGTAATATTTGATTTTCAGAAAGCCGATG 1396
Db 1116 AAGTCGAGATCGAAATTTCCCTCTCTAATTCACAAATTTTATCTGAACTAATCTCTGGACA 1175
Qy 1397 ATATAAAATTTACTTTCAATTTAGCTATCATGAACCTTAGTAGGAGAGACTACCGCTAGACCAGA 1456
Db 1176 ACATACGACTGCTACACAACTATTTTAGGGCGAATATATTTAGAGTAGATTTCTCAAG- 1234
Qy 1457 GTATCGGTTTCAAAGGCGAGATTTTCGTAGGGTAGGGGACCTGATTTAAATTTATGATGC 1516
Db 1235 --CTTGTAATTTAAATGATACCAATATGAGTGAATAGGGCGGTATTTTATCATGATGC 1292
Qy 1517 AGGTAATATGGGCTAAGCAGGATGACAAATGAAATCTACGTTCCCACTTGTATTTGCACTC 1576
Db 1293 GAGTGAAGGTTCTCAAGATCCGTC-----TACGAGGGGTATATTCGAA 1336
Qy 1577 TAATGTTGTAGAGGACCTCTCATAGATTTATCAAAATGGGCATGTTGTATATGAAA 1636
Db 1337 CAATCGGATAGATAACCC-----TAGAGTTCAAAATATTAACACTTATTTACCTGGAGA 1391
Qy 1637 CTCAGAGTTTAACTGATATGTTGGACACATACAAGTTTAAACCGTGAANAATATAATTGA 1696
Db 1392 AAATTCAGATATCCCAACTCCAGAGACTATATCTCATATATTAAGCACACAATAAATTT 1451
Qy 1697 AGCCAATCAAAATACACAAATACCGGGGTGAAGATTTATACCTTCAAAAATATCTTGC 1756
Db 1452 AACAGGAGGACTTAGACAAGTAGCATCTAATCCCGTTTCATCTTTAGTAATGATGGTTG 1511
Qy 1757 TAATGCTTATACCTATGTAATAAAGCACTATA--CAGGTGGGATTTAATCCGTTTT 1814
Db 1512 GACACATAAAGTCTGGCTCGTAAACAATACCATTAATCCAGATAGAAATTTACACAGATACC 1571
Qy 1815 TTAAGAACAAAATCAGAGTATAACGAGTTTATGCAAGGTGGCGGAATTAAGATTTATTT 1874
Db 1572 TTTAGTGAAGGATTTAGAGTTTGGGGGGCACTCTGTCTATTACAGGACGAGATTTTAC 1631
Qy 1875 AATAACAAAACCTCAGGACAAAGTTACCGTATTTCTGTTTTCGTTATGCTGCAGATAAGCT 1934
Db 1632 AGGAGGGATATCCTTCGAAGAAATACCTTTGCTGATTTTGTATCTCTACAAGTCAATAT 1691
Qy 1935 GCTTTCTTTAGTGTATATCTTTATCCAGGAGGTTGGGGTTCAAATCGTTTGTATCGCTT 1994
Db 1692 TAATTCACCAAT--TACCCAAAGATACCGTTTAAGATTTCTGTTACGTTCCAGTTAGGGATG 1750
Qy 1995 GAAAAATCTTACTCTGGAAATATAGCAATTTTAAATAATAGTGAATTTTAAATTCGCTGAA 2054
Db 1751 CAGGAGTTATAGTATTAAACAGGACGGCATCCACAGAGTGGGAGGCCAAGTTAGTGTA 1810
Qy 2055 ATTTATCACACCTCCATCTAGTTCAACATTTCAAGATGATGAGATGCAAGGGAAT 2114
Db 1811 AT-----ATGCTCTTCAGAAAACCTATGGAATAGGGGAGAACTTAAACATCT 1857
Qy 2115 AGTTTTCAATCAGATGTAAACGGTGTCTCGACAAAATTTGAATTCCTCCCAAGTAATACA 2174
Db 1858 AG--AACATTTAGATATACCGATTTTAGTAACTCTTTTTCATTTTAGGCTATCCAGATA 1915
Qy 2175 ACACTTTTGAATATAGGGGAGAACGGGACCTTAGAAAAACAAAGAACCGGTTGAACGAT 2234
Db 1916 TAAATGGGATAGTGAACAACTCTATTTTGGTGCAGGTTCTATTAGTAGCGGTGAACCTTT 1975
Qy 2235 CTGTTTACCATAATAACAAATAATTTACTAGAAATAGGTGGTATTGCTGTTTAA---CA 2291
Db 1976 ATATAGATAAAATTTGAATTTATTTCTAGCAGATGCAACATTTGAAGCAGAAATCTGATTTAG 2035
Qy 2292 AATAAGCGAAAAAGTTGTAGTCTTATGTTTACAAAGTAGTACGAAAAATACGTTTAAAAA 2351
Db 2036 AAAGAGCACAAAGGCGGTGAATGCCCTGTTTTACTTCTTCCATCAATCGGTTTAAAA 2095

Qy 2352 TAGAAAAACGACAGATTTATGAATTAGATCAAGCGGCCATTTCTTATAGAAATGTATGTAGATG 2411
Db 2096 CCGATGTGACGGATTTATCATATTGATCAAGTATCAAAATTTAGTGATTTGTTTATCAGATG 2155
Qy 2412 AAAAAATCTCTCAGGAAAAAATAATGTTATGGGATGAATAAATCTGCAAAACAACTTTA 2471
Db 2156 AATTTTGTCTGGATGANAAGCGAGAAATTTGTCGAGANAAGTCAAAATCGAAGACGACTCA 2215
Qy 2472 GTCACTCTGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGATTTGGACATTCGGTA 2531
Db 2216 GTGATGAGGGGAAATTTACTTCAAGATCCAACTTCAGAGGGATCAATAGACAAACAGACC 2275
Qy 2532 ATGATATTTATCATAGGATCCAAATAATCTTATTTTAAAGGAAAAATTTCTACAGATGCGTG 2591
Db 2276 GTGGCTGGAGAGAAAGTACAGATATTAACATCCAAAGGAGGATGACGTTATTTCAAAGAGA 2335
Qy 2592 GAGCAGGAGACATATATGGAATCTCT-----ATTTCCAACTTATCTGTCAAAAA 2642
Db 2336 ATTACGTCACTACCGGTACCGTTGATGAGTGTCTTCAACGTTATTTATATCAGAAAA 2395
Qy 2643 TAGATGAGTCTAAATTTAAAAACCATATACACGTTATCGAGTAGAGGGTTTGTGGGAAGTA 2702
Db 2396 TAGATGAGTCGAAATTTAAAGCTTATACCGTTATGAATTAAGAGGGTATATCGAAGATA 2455
Qy 2703 GTAAAGATTTGAAATTAATGTTAAACGTTACGTTAGGGAAAAAATGATGCTATCATGAATG 2762
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Qy 2763 TTTCAAAATGATTTGGCCTTATATGACGCTTAATCTTCTATGTTGGAGATTTATCGCTGAT 2822
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Qy 2823 CATCTCTCAGTATGTCGACCAAGGGTATCTTACACCAACAGATGGATGCTATGCTCCGATA 2882
Db 2573 AACCGAATCGATCG-----CGCCACACCTTGAATGGAATCTGATC 2614
Qy 2883 TGTATGCAATGCCCCGAAATATAGATAGAAAGCATGTGAAAGTGTCAAGTCTGATCTCAT 2942
Db 2615 TAGATTTGTTCTTCGACAGACGCGGAAAAA-----TGTGCAATCATTTCCCATCAT 2665
Qy 2943 TTTGATTTTCAATTTACACCGGAGAGTAGATACAAATACAAATGCTAGTATTTGATGCT 3002
Db 2666 TCACCTTGGATATGATGTTGGATGTAAGACTTAAATAGGACTTTAGTGTATGGGTGA 2725
Qy 3003 TATTAATAATTTCTAATCCAGATGATAGCTTACAGTAGTAGGGAATCTAGAAAGTCAATTGAAG 3062
Db 2726 TATTCAGATTAAGACGCAAGATGCCATGCAAGACTAGGGAATCTAGAGTTTCTCGAAG 2785
Qy 3063 AAGGACCTAAACAGGTGAAGCATTTGGCACATGTGAAAACAAAGAAAAAGAAATGGAAC 3122
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Qy 3123 AACACATGGAGAAAAACGTTGGGAAACACACAGCCTATGATCCAGCAAAACAGGCTG 3182
Db 2846 ACAACGAGAGAAACTGCAAGTTGGAACAAATATTTGTTTAAAGAGGCAAAAGAAATCTG 2905
Qy 3183 TAGATGCAATTTATTAATAATGAACAGAA-----GTTACACTTATCATATTTACTTTAGATC 3236
Db 2906 TAGATGCTTTATTTGTAAACTCTCAATATGATAGATTACAAGTGGATACGAACATCGCA 2965
Qy 3237 ATATTTAAAAACGCTGATCGATGGTACAGTCCCTATGTATACCAATATTTGTTTAC 3296
Db 2966 TGAATCATGCGGCAGATAAACCGGTTTATAGAAATCCGGGAAGCGTATCTGCCAGAGTTGT 3025
Qy 3297 CGAATGCTCCAGGTATGAATATGATGATATCAAGAGTTAAACCGCACGCTATCATGCAAG 3356
Db 3026 CTGTGATTTCCAGGTGTCAATGCGGCCATTTTCGAAGAATTAGAGGAGCGTATTTTACAG 3085
Qy 3357 GTTATATTTATATGATGACGAAATGTCAACAAATGGTGTGACTTTTACACAGGATTTAC 3416
Db 3086 CGTATTTCTTATATGATGCGAGAAATGTCAATTTAAAAAATGGCGATTTTCAATATATGGCTTAT 3145

Qy	3417	AGGATGGCAGC	CAACAGGAAATCCCGGTACAA	---CAAT	TGGATGGAGCTTCAGTAT	3473
Db	3146	TATGCTGGAA	CGTGAAGGTCATG	TAGATAGAGAGCAAAACAC	CCCGTTCCGTCC	3205
Qy	3474	TAGTTCTATCAAA	TTGGAGCGCGGGGTATCTCAAA	ACTTGCATGCTCAAGATCATCATG		3533
Db	3206	TTGTTATCCAGAT	TGGAGCGAGAGTGTCACA	AGAGGTTCTGTCTCTCCAGGTCGTG		3265
Qy	3534	GATATGTTACGTGTG	ATTGCCAAAAGGAGGACCTCGAAA	AGGGTATGTAAACCATGA		3593
Db	3266	GCTATATCCTT	CGTGTACAGCATATAAAGAGGGATATGAGAGGGCTCGTAA	CGATCC		3325
Qy	3594	TGGATTGTAATGGA	AACGAGAAACCTTAA	GTTCACCTTCTTCGGAAGAAG		3644
Db	3326	ATGAGATCGAAG	ACAATATACAGACGAATCGAAATTCAGCA	ACTGTGTAGAAG		3376

RESULT 14

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US-07-973-320-3
; Sequence 3, Application US/07973320
; Patent No. 5286486
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Fu, Jenny M.
; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,320

```

Query Match 5.1%; Score 305.4; DB 2; Length 3414;
Best Local Similarity 53.6%; Pred. No. 1.9e-58;

Matches	809;	Conservative	0;	Mismatches	616;	Indels	84;	Gaps	5;
Qy	2292	AATAAGCGAAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA	2351						
Db	1940	AAAAAGCACAGAAGCGGTGAATACCTTGTTTACAGAGG--AAGAAATGCATCTCAAA	1996						
Qy	2352	TAGAAACGACAGATTATAGAAATAGATCAAGCGGCCATTTCTTATAGAAATGTATGTCCAGATG	2411						
Db	1997	AAGACGTGACAGATTATAAAGTGGACGAGTTTCAATTTTAGTGGATTGTATATCAGGGG	2056						
Qy	2412	AACAAAATCCTCAGGAAAAAATAATGTATGGGATGAAATAAAACTGGCAAAACAACACTTA	2471						
Db	2057	ATTTATATCCCAATGAGAAACGCGAACTCAAAAATCTAGTCAAAATACGCAAAACGTTTGA	2116						
Qy	2472	GTCAAGTCCTGTAATCTACTCCAAAATGGAGACTTTCTCGGGAATGATGGACATTCGGTA	2531						
Db	2117	GCTATTTCCCGTAATTTACTTCTAGATCCACATTCGATTCATTAAATTCATCTGAGGAGA	2176						
Qy	2532	ATGATATTTATCATAAGGATCCAATAATCTCTATTTTTTAAAGGAAAAATTTCTACAGATCGGT-	2590						
Db	2177	ATCGTTGGTATCGAAGTAATGGTATTGTGATTGGAAATGGGGATTTTGTATTCAAAGGTA	2236						
Qy	2591	-----GGAGCAGCAGACATATATGGAACTCTATTTCCAACTTATCTGTCAAAATAA	2642						
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Db	2858	AAATTCGGGCTCGCAAGAAAGATTGTCCTAATCAATACGCGAAGGTTATGTCTATGTTTAT	2917						
Qy	3297	CGAATGCTCCAGGTATGAACATATGATGTATATCAAGAGTTAAACCGCACGTATCATGCAAG	3356						
Db	2918	CTGTGTTTCAGGTGTAATTCACCTTATTTTACAGATTTAGTGAAGCAGTACACACGAG	2977						

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QY 2978 CATTTCAATATATGATGATACGAAATGTTGTGCGTAATGGTCGATTCCTCAATGGCTTAT 3037
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QY 3417 AGGGATGGCAGCAACAGGAAATGCCCGGTACAAACAATGGATGGAGCTTCAGTATTAG 3476
Db |||||
QY 3038 CCGATTGGAATTTGAACATCTGACGTTAAAGGTACAAAGAGAAATGGGAATAACGTTATTAG 3097
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QY 3477 TTCTATCAATTTGGAGCGGGGGGTATCTCAAACTTGCATGCTCAAGATCATCTATGGAT 3536
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QY 3158 ATATCTTACGTGTAAACAGCGCGCAAGATAGGAATTTGGGAAGGATATATAACGATTACGG 3217
Db |||||
QY 3597 ATTGTAATGGAAGCAGGAACACTTAAGTTCACTTCTTCCGAGAA----- 3643
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QY 3218 ATGAAGAAGGCATACAGTTCATTTGAGATTTTACTGCTGATGTGAAGTGTGATGCACTA 3277
Db |||||
QY 3644 -----GGATATATGACAAAAACAGTAGAGGTATTCCAGAAAGTGATCGTG 3689
Db |||||
QY 3278 ATGCGTTTATATCCGTTTATATTACAAAGAACTGGAATTTCTCCAGATACAGAAAG 3337
Db |||||
QY 3690 TAGCGATTGAATAGAGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTTT 3749
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QY 3750 GTATGCAAG 3758
Db |||||
QY 3398 TGATGGAAG 3406
Db |||||
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RESULT 15

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US-07-973-320-1
; Sequence 1, Application US/07973320
; Patent No. 5286486
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Fu, Jenny M.
; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,320
; FILING DATE: 19921106
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/788,638
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA68.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3414 base pairs
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; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: dakota
; INDIVIDUAL ISOLATE: HD511
; IMMEDIATE SOURCE:
; LIBRARY: Landagem (TM)-11 library of J.M. Fu
; CLONE: 511
; US-07-973-320-1
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Best Local Similarity 53.5%; Pred. No. 9.9e-58;
Matches 807; Conservative 0; Mismatches 618; Indels 84; Gaps 5;

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QY 2472 GTCAGTCTGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGATTTGGGAATTCGGTA 2531
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QY 2117 GCTATTCCGTAATTTACTTCTAGATCCCACTTCGATTTCTATTAATTCATCTGAGGAGA 2176
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QY 2532 ATGATATTATCATAGGATCCAATAATCCTATTTTAAAGGAAAAATTTCTACAGATCGGT- 2590
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QY 2177 ATGGTTGGTATGGAAGTAATGGTATTTGTTGTTGGAATGGGGATTTTGTATTTCAAGGTA 2236
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QY 2591 -----GGAGCAGCAGACATATATGGAACCTCTATTTCCAACTATATCTGTCAAAAAA 2642
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QY 2237 ACTATTTAATTTTTCAGGTACCAATGATACACATATATCCAATATCTCTACCAAAAAA 2296
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QY 2703 GTAAAGATTGAAATTAATGTTAACAACGTTACGGGAAAGAAATTCATGCTATCATGAATG 2762
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Job time : 704.153 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 12:54:35 / Search time 6793.75 Seconds
(without alignments)
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Perfect score: 2082
Sequence: 1 gtgaaaagatgagtcata.....acgatctgttaccataa 2082

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
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- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
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- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	2073	99.6	2073	6	CQ868314 Sequence
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5	825.4	39.6	4100	1	AB112346 Bacillus
6	747.2	35.9	2019	6	CQ868325 Sequence
7	747.2	35.9	2145	6	CQ868324 Sequence
8	739.8	35.5	2010	6	CQ868327 Sequence
9	204.8	9.8	2028	1	BTU88189
10	168.6	8.1	3468	6	AR143378 Sequence
11	168.6	8.1	3468	6	AR567184 Sequence
12	168.6	8.1	3471	6	BD062618 Toxins
13	168.6	8.1	3471	6	BD128371 Toxin act
14	168.6	8.1	3471	6	AR205863 Sequence
15	168.6	8.1	3471	6	AR339971 Sequence
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22	160.6	7.7	2407	6	AX098659 Sequence
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ALIGNMENTS

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LOCUS 2082 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 13 from Patent WO2004074462.
ACCESSION CQ868312
VERSION CQ868312.1 GI:51998358
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 13 02-SEP-2004;
Athenix Corporation (US)
FEATURES
Location/Qualifiers
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/db_xref="GI:51998359"
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LVYFKLSERDFNEIGSLSRNAQVLLPFPQAQNVQLLRLLRDAVQTKAQGFPL
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ORIGIN

Query Match 100.0%; Score 2082; DB 6; Length 2082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1381 GAACTCTAGTTCCTCACTTGTATGTCACCTTAATGTTGTAGAGGACCTCTCATAGATTA 1440
QY 1441 TCAAAATCGGCAATGTTGTATATGGAACCTCACAGTTTAAACGATATATGTTTGGACACAT 1500
DB |||||
1441 TCAAAATCGGCAATGTTGTATATGGAACCTCACAGTTTAAACGATATATGTTTGGACACAT 1500
QY 1501 ACAAGTTTAAACCGTGAATAATAATGAAGCCAAATCAAAATACACAAATACCGCGGTG 1560
DB |||||
1501 ACAAGTTTAAACCGTGAATAATAATGAAGCCAAATCAAAATACACAAATACCGCGGTG 1560
QY 1561 AAGAGTTTATACCTTCAAAATTTATCTGCTAATGCTATACCTATGTAATAAAGGCACCT 1620
DB |||||
1561 AAGAGTTTATACCTTCAAAATTTATCTGCTAATGCTATACCTATGTAATAAAGGCACCT 1620
QY 1621 CATACAGGTGGGATTTAATCGTGTGTAAGAAACAAATCAGAGTATAACGAGTTTAT 1680
DB |||||
1621 CATACAGGTGGGATTTAATCGTGTGTAAGAAACAAATCAGAGTATAACGAGTTTAT 1680
QY 1681 GCAGTGGCGGAATTTAGATTGATTAATAACAAACTGACAGGACAAAGTTTACCGTAT 1740
DB |||||
1681 GCAGTGGCGGAATTTAGATTGATTAATAACAAACTGACAGGACAAAGTTTACCGTAT 1740
QY 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
DB |||||
1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
QY 1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAATAATCTTACTCTGGAATTTATGACGATTTA 1860
DB |||||
1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAATAATCTTACTCTGGAATTTATGACGATTTA 1860
QY 1861 AAATATAGTGAATTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAACAT 1920
DB |||||
1861 AAATATAGTGAATTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAACAT 1920
QY 1921 CAGATGGATGCGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACGTTCTTCGAC 1980
DB |||||
1921 CAGATGGATGCGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACGTTCTTCGAC 1980
QY 1981 AAAATTGGAATTCCTCCCAAGTAATAACAACTTTTAGAATATGAGGGAGAACGGGACCTTA 2040
DB |||||
1981 AAAATTGGAATTCCTCCCAAGTAATAACAACTTTTAGAATATGAGGGAGAACGGGACCTTA 2040
QY 2041 GAAAAACAAAGAACCGCGGTGAACGATCTGTTTACCAATTA 2082
DB |||||
2041 GAAAAACAAAGAACCGCGGTGAACGATCTGTTTACCAATTA 2082

RESULT 2	Q868311	5980 bp	DNA	linear	PAT 14-SEP-2004
LOCUS	Q868311	Sequence 12 from Patent WO2004074462.			
DEFINITION	Q868311				
ACCESSION	Q868311.1	GI:51998357			
VERSION					
KEYWORDS	Bacillus thuringiensis				
SOURCE	Bacillus thuringiensis				
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.				
REFERENCE	1				
AUTHORS	Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B.				
TITLE	Delta-endotoxin genes and methods for their use				
JOURNAL	Patent: WO 2004074462-A 12 02-SEP-2004;				
	Athenix Corporation (US)				
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	Best Local Similarity 100.0%; Pred. No. 0;				
	Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	228	AATAACAAATAACGCCAACACAGATATCCTTTTGCAGAAATATCGGGATATGCTACTATG	287		
Qy	121	TCCTGGAAATGATGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA	180		
Db	288	TCCTGGAAATGATGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA	347		
Qy	181	ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTCGGTGGAAATTAAT	240		
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Db	408	ACACTATTATCAATAATAGGAAACCTAATTCGCACTAATCGTCAAACTGTGTGAGCACTT	467		
Qy	301	TCCTATATGATTTATATCTATATATTCGTAAGAGGATAGCGATAGTGTGTTTAAGTGAT	360		
Db	468	TCCTATATGATTTATATCTATATATTCGTAAGAGGATAGCGATAGTGTGTTTAAGTGAT	527		
Qy	361	CGGATTGCGAGATTTTCAGCGTAAATTTGAAATAATATAGAGAGTATTAATCTTTCTTATCTT	420		
Db	528	CGGATTGCGAGATTTTCAGCGTAAATTTGAAATAATATAGAGAGTATTAATCTTTCTTATCTT	587		
Qy	421	GGGGCTTGGCTTAAAGACCGGTAAACCCACTTCAAAAGACAAATAATTCGTATATCGGACAA	480		
Db	588	GGGGCTTGGCTTAAAGACCGGTAAACCCACTTCAAAAGACAAATAATTCGTATATCGGACAA	647		
Qy	481	TTAGTTTATTTATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCATTG	540		
Db	648	TTAGTTTATTTATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCATTG	707		
Qy	541	TCAAGAAACAACTGCTCAAGTATTTGTTATPACCTACTTTTGGACAAGCTGCAAAATGTCGAG	600		
Db	708	TCAAGAAACAACTGCTCAAGTATTTGTTATPACCTACTTTTGGACAAGCTGCAAAATGTCGAG	767		
Qy	601	TTATTACTATTAAGGATGTCAGTTCAATATAAAGACACAAATGGTCCCAATTTTTCAGGTGCA	660		
Db	768	TTATTACTATTAAGGATGTCAGTTCAATATAAAGACACAAATGGTCCCAATTTTTCAGGTGCA	827		
Qy	661	GAGAAATGTAAGATCGGAAATTAATATCACTAAACAGTGGTGTGATTTTACCGGTGATTAC	720		

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Qy 1210 GATTTTCAGATCCGATGATATAAATAATCTCTTACCTATCATGAACCTAGTAGGA 1269
Db 1201 GATTTTCAGATCCGATGATATAAATAATCTCTTACCTATCATGAACCTAGTAGGA 1260
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Db 1261 GAGACTACCGCTAGACAGAGTAGTCGTGTTTCAAAGGCAGATTTTCCGTAGGGTAGGGGGA 1320
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Db 1921 GTGGAGATCAAGCGAATAGTTTTCATCAGATGTAACGTGTTCTCGACAAATTTGAA 1980
Qy 1990 TTCTCTCCAGTAAATACAACTTTTGAATATGAGGAGAACCGGACCTAGAAAAACA 2049
Db 1981 TTCTCTCCAGTAAATACAACTTTTGAATATGAGGAGAACCGGACCTAGAAAAACA 2040
Qy 2050 AAGAACCGGTGAACGATCTGTTTACCAATTA 2082
Db 2041 AAGAACCGGTGAACGATCTGTTTACCAATTA 2073

RESULT 4

AB074414
LOCUS
DEFINITION
Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.
AB074414
AB074414.1 GI:16945771
Bacillus thuringiensis serovar aizawai

ORGANISM

Bacillus thuringiensis serovar aizawai
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE

AUTHORS

TITLE

Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 3746)

AUTHORS

Ito, T., Sahara, K., Asano, S. and Bando, H.

TITLE

Direct Submission

JOURNAL

Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Kita-9jyou Nishi-9chome, Kita-ku Sapporo-shi, Hokkaido 060-8589, Japan (E-mail: ito-t@abs.agr.hokudai.ac.jp, tel:81-011-716-2487)

FEATURES

source

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AFNTLEANGTRCGPLVWLRSIGLYNEVYVRVPSGVTGRHEDYTTGNPFQMSGT

TSNDLRDISFNSDIFKESKALMNLVNAARPEYRVSRAEFSESTAIYLLDAGNS

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GLSDTNTNIGDVLFKISNPDPDTLGNVEEGLPTGEGALTHVQKREKKQKHWK

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ORIGIN

Query Match

Best Local Similarity

Matches 1386; Conservative

59.3%; Score 1234.2; DB 1; Length 3746;

88.4%; Pred. No. 1.1e-212;

Mismatches 173; Indels 8; Gaps 4;

Qy 12 GAGTCATATCAAAATAAATAATGAATATGAAATATTGGAATCTCTCATCAATAACAA 71

Db 1 GAATTCATATGAAATAAATAATGAATATGAAATATTGGAATCTCTCATCAATAACAA 60

Qy 72 TAGCCCAACAGATATCTCTTTTGCATAAATAATCGGGATATGCTCTACTATGCTTGGATGA 131

Db	61	TATGCCAAACAGATATCTCTTTTGCAAATGATCGGGATATGTCTACTATGTCTTTCAATGA	120
Qy	132	TTGTCCAGGAAATCTCATGGGATGAAATTTTCGGGAATCAGTGCAGAACGATAACAAGTATTGG	191
Db	121	TTGTCAAGGAATCTCATGGGATGAAATTTTCGGGAATCAGCCGAAACGATAACAAGTATTGG	180
Qy	192	GATAAATCTTTATAGAGTTTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTATC	251
Db	181	GATAGATCTTTATAGAGTTTTTGATGGAACTAGTTTGGGTGGAAATTAATACACTATTTTC	240
Qy	252	AATAATAGGAACACTAATTCGGACTAATCGTCAAACGTGTGACGACTTTCTATATGTGA	311
Db	241	AATAATAGSAAAACTAAATTCGGACTAATCATCAATCTGTGTGACGACTTTCTATATGTGA	300
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Qy	848	GTAGAGAAATCAGTTGGCGGTATTGATATATTCGTATATTTCCAATTAATGATTTTG	907
Db	840	GTAGAGAAATGACGTTGACCGTATTGATATTATCGCTATATTTCAAACTTATGATTTCA	899
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Qy	968	GATATTCAATCGGGAACCTTATAGTTGGTTACGGAAATGCGCCTTAATPACTTTTAAATGGGTTAG	1027
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AB112346			
LOCUS	AB112346	4100 bp DNA linear BCT 14-JUN-2003	
DEFINITION	Bacillus thuringiensis serovar aizawai cry40-like and ORF2 genes for putative mosquitocidal toxin, hypothetical protein, complete cds.		
ACCESSION	AB112346		
VERSION	AB112346.1	GI:31745043	
KEYWORDS	Bacillus thuringiensis serovar aizawai		
SOURCE	Bacillus thuringiensis serovar aizawai		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1	Ito, T., Sahara, K., Asano, S. and Bando, H.	
AUTHORS	Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding Mosquitocidal Proteins		
TITLE	Unpublished		
JOURNAL	2	(bases 1 to 4100)	
REFERENCE	Ito, T., Sahara, K., Asano, S. and Bando, H.		
AUTHORS	Direct Submission		
TITLE	Submitted (12-JUN-2003) Takeshi Ito, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience; Kita-9jo, Nishi-9chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan		
JOURNAL	(E-mail: ito-t@abs.agr.hokudai.ac.jp. Tel: 81-11-706-2487 (ex.2487))		
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CDS

ORIGIN

Query Match 39.6%; Score 825.4; DB 1; Length 4100;

Best Local Similarity 66.5%; Pred. No. 5.1e-139;

Matches 1406; Conservative 0; Mismatches 571; Indels 138; Gaps 10;

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DB 330 AATAACAAATATACCAAAACAGATATCCTTTTGGCAAAATGATCGGATATGCTCTCTATG 389
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DB 390 TCTTGGAAATGATGTGAGGGAATCAGGAGATGATGAGGGAATCAACCGGAGTTTC 449
QY 181 ACAAGTATGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240
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Qy 1708 AATAACAAAACGACGACAAAGTTACCGTATTCGTTTTCGTTATGCTGCGAATAAGCT 1767

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Db 1983 TGCCAAATTAGCCATGAGGAGTGGCGAGGAGGCCCGGTT---ATGTACAAGACACGT 2039

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Db 2100 ATATTACTATGCTCGGAAGATTATATCTTTTGTGTTG-----ACGATA 2144

Qy 1948 AGTTTTCAATCAGATGTAACGTTGTTCTCGACAAATTTGAATTCCTCCCAAGTAAATACA 2007

Db 2145 GACCTTGAAGTGGTGAGCTCTTTATATCGACAAATTTGAATTTATCCAGATGATTTA 2204

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RESULT 6

LOCUS Q0868325 2019 bp DNA linear PAT 13-SEP-2004

DEFINITION Sequence 26 from Patent WO2004074462.

ACCESSION Q0868325

VERSION Q0868325.1 GI:51998371

KEYWORDS Bacillus thuringiensis

SOURCE Bacillus thuringiensis

ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1

AUTHORS Carozzi, N., Hargiss, T., Koziel, M. G., Duck, N. B. and Carr, B.

TITLE Delta-endotoxin genes and methods for their use

JOURNAL Patent: WO 2004074462-A 26 02-SEP-2004;

Athenix Corporation (US)

FEATURES

source Location/Qualifiers

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Query Match 35.9%; Score 747.2; DB 6; Length 2019;

Best Local Similarity 69.8%; Pred. No. 8.1e-125;

Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

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Db 181 GTAACTATTTGGACATACCTTATACAAATCTTGTCTAGAACCCGGTATAGTGGAAATCTCT 240

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LOCUS 2145 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 25 from Patent WO200407462.
ACCESSION CQ868324
VERSION CQ868324.1 GI:51998370
KEYWORDS Bacillus thuringiensis
SOURCE Bacillus thuringiensis
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 200407462-A 25 02-SEP-2004;
Athenix Corporation (US)
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Best Local Similarity 69.8%; Pred. No. 8e-125;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

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RESULT 8
CQ868327
LOCUS CQ868327 2010 bp DNA linear PAT 13-SRP-2004
DEFINITION Sequence 28 from Patent WO2004074462.
ACCESSION CQ868327
VERSION CQ868327.1 GI:51998373
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1
AUTHORS Carozzi N., Hargies, T., Koziel M.G., Duck N.B. and Carr, B.
TITLE Delta-endotoxin genes and methods for their use
JOURNAL Patent: WO 2004074462-A 28 02-SEP-2004;
Athenix Corporation (US)
FEATURES
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ORIGIN
Query Match 35.5%; Score 739.8; DB 6; Length 2010;
Best Local Similarity 69.7%; Pred. No. 1.e-123;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;
QY 10 ATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCGAATAACACA 69
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RESULT 9

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BTU8189
LOCUS 2028 bp DNA linear BCT 01-OCT-1998
DEFINITION Bacillus thuringiensis jegathesian insecticidal protein Jeg74 gene,
complete cds.
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ACCESSION U88189
VERSION U88189.1 GI:3668334
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KEYWORDS
SOURCE
ORGANISM Bacillus thuringiensis serovar jegathesian
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
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REFERENCE
AUTHORS 1 (bases 1 to 2028)
TITLE Kawalek,M.D. and Gill,S.S.
Isolation and characterization of insecticidal genes from Bacillus
thuringiensis subsp. jegathesian
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JOURNAL
REFERENCE 2 (bases 1 to 2028)
AUTHORS Kawalek,M.D. and Gill,S.S.
TITLE Direct Submission
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JOURNAL

Submitted (29-JAN-1997) Entomology, University of California, 5419
Boyce Hall, Riverside, CA 92521, USA
Location/Qualifiers

FEATURES

source

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ORIGIN

Query Match 9.8%; Score 204.8; DB 1; Length 2028;
Best Local Similarity 55.5%; Pred. No. 4.8e-27;
Matches 545; Conservative 0; Mismatches 392; Indels 45; Gaps 6;

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RESULT 10
ARI43378
LOCUS ARI43378 3468 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6204246.
ACCESSION ARI43378
VERSION ARI43378.1 GI:15104664
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3468)
AUTHORS Bosch,H.Jan. and Stiekema,W.Johannes.
TITLE Hybrid toxin
JOURNAL Patent: US 6204246-A 9 20-MAR-2001;
FEATURES
source Location/Qualifiers
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ORIGIN
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Best Local Similarity 52.5%; Pred. No. 1.3e-20;
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RESULT 11
ARI567184
LOCUS ARI567184 3468 bp mRNA linear PAT 08-OCT-2004
DEFINITION Sequence 9 from patent US 6780408.
ACCESSION ARI567184
VERSION ARI567184.1 GI:53984827
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3468)
AUTHORS Bosch,H.J. and Stiekema,W.J.
TITLE Genes encoding hybrid bacillus thuringiensis toxins
JOURNAL Patent: US 6780408-A 9 24-AUG-2004;
Syngenta Participations AG; Schwaarzwalldallee;
GBX;
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source Location/Qualifiers
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ORIGIN
Query Match 8.1%; Score 168.6; DB 6; Length 3468;
Best Local Similarity 52.5%; Pred. No. 1.3e-20;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
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DB 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAAATAG 980

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ACCESSION
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JP 2001507208-A/42.
KEYWORDS
Homo sapiens (human)
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Hominidae; Homo.
1 (bases 1 to 3471)
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Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A.
AUTHORS
Toxins active against pests
TITLE
Patent: JP 2001507208-A 42 05-JUN-2001;
JOURNAL
MYCOGEN CORP
COMMENT
FN JP 2001507208-A/42
PD 05-JUN-2001

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 52.5%; Pred. No. 1.3e-20;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTTGGGAATCAGTCGAAACGATAACAAGTATTTGGGATAAACTTTATAGAGTTTGTGAT 215
DB 153 AATAGCGGATGCAAGCAAAAGAACGAGTATCTATTTGGGACAAACCATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT 269
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QY 750 GTATACCAATTAATTTTATTTGATATAGTATAGTATAGTTTAAATCAGATTAATAACAGGGGG 809
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DB 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATGGGTTTGTATCATCGTAGTAGTCT 947
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BRIAN A STOCKHOF
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Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.

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ACCESSION			
VERSION			
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ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
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Best Local Similarity		52.5%;	Pred. No. 1.3e-20;
Matches		458;	Conservative 0; Mismatches 364; Indels 51; Gaps 2;
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Matches		458;	Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY	156	AAATTTGGGAATCAGTCGAACGATAACAAGTATTGGGATAAATCTTTATAGAGTTTGTGAT	215
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Db	828	ATTAGATATATAGTACATCATTTTCAAGTCTTGATATTACTAATTAACCAATAGAAACACA	887
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Db	888	TTTTTCAGTTGAGTAGGGTCAITTTATACAGATCCAAATGGTTTGTGTACATCGTAGTAGTCT	947
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ORGANISM Unknown.
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AUTHORS Schnepf,H.E., Wicker,C., Narva,K.E., Walz,M. and Stockhoff,B.A.
TITLE Toxins active against pests
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Mycogen Corporation; Indianapolis, IN
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Db 573 ACCTCTCTTTGCGAGCGCTGCAATTTTCCATTTTATTAAGGATGCTACTAGATA 632
Qy 630 TAAAGCACAATGGTTCCTCAATTTTGAAGTCAGAGAAATGTAAGATCGGAATTTAATATCACC 689
Db 633 TGSCACTAAATGGGGGCTATACAACTGCTACACCTTTTAAATTTCAATCAAAACTAGT 692
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Qy 750 GTATACCAATATTGTTTATATTGGTATCAGGTAGGTTTAAATCAGATATAAAGAGGGGG 809
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Db 828 ATTAGATATAGTAGCATCTTTCAAGTCTTGATATTACTTAATCCCAATAGAAACAGA 887
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Db 888 TTTTCAGTTGAGTAGGCTATTTATACAGATCCAAATGGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGGAATTTGGCCTAATCTTTTAATGG 1022
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Job time : 6802.75 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:03:30 / Search time 5119.26 Seconds
(without alignments)
19028.273 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaaagatgagtcata.....acgatctgtttaccaattaa 2082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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8: gb_est8:*
9: gb_est9:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	54	2.6	1101	CNS000D1	AL065414 Drosophila
C 4	53	2.5	1101	CNS000B7	AL069440 Drosophila
C 5	52.8	2.5	874	AZ533618	AZ533618 ENTAC45TF
C 6	52.2	2.5	1101	CNS000EVL	AL069706 Drosophila
C 7	51.6	2.5	1101	CNS0010X	AL098379 Drosophila
C 8	51.2	2.5	1101	CNS000EA9	AL068837 Drosophila
C 9	50.6	2.4	548	BI502178	BI502178 kt86c11.y
C 10	50.6	2.4	1101	CNS017KX	AL108171 Drosophila
C 11	50.2	2.4	486	2	BG227627
C 12	50.2	2.4	520	2	BG227279
C 13	50	2.4	964	10	CNS0006N9
C 14	49.8	2.4	923	9	BH152435
C 15	49.6	2.4	892	9	AZ683446
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C 17	49.4	2.4	1225	10	CNS0161D
C 18	49.2	2.4	1001	10	CNS01400
C 19	48.6	2.3	1101	CNS000FV	AL071298 Drosophila
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C 22	48.2	2.3	1101	10	CNS017ZQ

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C 24	47.8	2.3	893	10	CNS013XE
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C 26	47.8	2.3	996	9	BH137139
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C 28	47.6	2.3	1101	10	CNS00EVL
C 29	47.4	2.3	862	10	CW954723
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C 37	46.4	2.2	1027	10	CNS02T50
C 38	46.4	2.2	1101	10	CNS00Z62
C 39	46.4	2.2	1225	10	CNS0161D
C 40	46	2.2	834	10	CNS008CK
C 41	46	2.2	1101	10	CNS017KE
C 42	45.8	2.2	612	9	AZ523655
C 43	45.8	2.2	863	9	AZ692735
C 44	45.6	2.2	886	9	AZ672805
C 45	45.6	2.2	963	10	CNS00A4L

ALIGNMENTS

RESULT 1
CNS0039G/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063921 GI:4941778

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammossier in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1. .1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR08K10"

/clone_lib="RPCI-98"

/note="end : TET3"

filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

```

1.1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
/note="end : T7"

```

ORIGIN

[illegible]

RESULT 7
CNS0100X

CNS0100X 1101 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BAC03G04 of DrosBAC library from *Drosophila melanogaster* (fruit
fly), genomic survey sequence.

AL098379.1 GI:5609990
AL098379
AL098379.1 GI:5609990

GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

CNS000EA9
LOCUS
DEFINITION
1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence, FET3 end of BAC #
BACR26K21 of RCI-98 library from *Drosophila melanogaster* (fruit
fly), genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
AL068837
AL068837.1 GI:4949081
GSS.

RESULT 9	BI502178	LOCUS	548 bp	mRNA	linear	EST 29-AUG-2001
DEFINITION	kt86c11.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter					
	Strongyloides ratti cDNA 5' similar to TR:Q18989 Q18989 D2045.9					
	PROTEIN [1] ; mRNA sequence.					
ACCESSION	BI502178					
VERSION	BI502178.1	GI:15352567				
KEYWORDS	EST.					
SOURCE	Strongyloides ratti					
ORGANISM	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloidea; Strongyloidea; Strongyloidea.					
REFERENCE	1 (bases 1 to 548)					
AUTHORS	McCart, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schur, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.					
TITLE	The Washington Univ. Nematode EST Project, 1999					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: McCarter JP The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmcarter@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. High quality sequence stop: 395.					
FEATURES	Location/Qualifiers					
source	1..548					
	/organism="Strongyloides ratti"					
	/mol_type="mRNA"					
	/db_xref="taxon:34506"					
	/dev_stage="L2"					
	/lab_host="DH10B"					
	/clone_lib="Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter"					
	/note="Vector: pAMP1 (Gibco); The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Mark Viney of Bristol, UK."					
ORIGIN						
Query Match	2.4%	Score 50.6;	DB 3;	Length 548;		
Best Local Similarity	44.9%;	Pred. No. 0.56;				
Matches	191;	Conservative 0;	Mismatches 234;	Indels 0;	Gaps 0;	
Qy	253	ATAATAGGAAAACTAAATCCGACTAATCGTCAAACTGTGTCAGCACATTTCTATATGTGAT	312			
Db	114	ATATTAAATAGAACCTATTATATAAATTTAAAAAATGGATTCTTACTTAAACATTT	173			
Qy	313	TTATTATCTAAATTCGTAAGAGAGGTAGCCGATAGTGTGTTTAAGTGATGCGATTCGAGAT	372			
Db	174	GAAGAAAGATAACATTTAGAAATGTTTGATTAAGATTTCTAATGAATTTGAGGTATTCCTTCAT	233			
Qy	373	TTTGACGGTAAATTCGAAAAATTTATAGACAGTATTATCTTTCTTATCTTGGGGCTTGGCTT	432			
Db	234	TCAGCTAAATTAATGAATATTCATTTATATCAATTAATCAATTAATTAATTAATTAATTAAT	293			
Qy	433	AAAGACGGTAAACCACTTTCAAAAGACAAATAATTTCTGATATCGGCAATTAATTAATTAAT	492			
Db	294	TTTGACTATGAAATTTAGAAAAAATCGAAGAGAGATTTAAATTAATTTATTTGTTGCT	353			

has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."

ORIGIN

Query Match 2.4%; Score 50.2; DB 2; Length 486;
Best Local Similarity 50.6%; Pred. No. 0.69;
Matches 121; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 344 ATAGTGTGTTTAAGTCGATGCGATTGTCAGATTTTGACGGTAAATTTGAAAAATTTATAGAGCT 403
DB 105 AGATTGATTCATAGAAAATGAATTAGAAGGTGGTGTATTATATAAAAATTTTAGAATA 164
QY 404 ATTATCTTTCTTATCTTGGGCTTGAAGACGGTAAACCCACTTCAAAAGACAAATA 463
DB 165 TAGACAAGTCAAGTAATAGTAATTCAGATTCAGATGTCAGAACAAATAATACAAATG 224
QY 464 ATTCGATATCGCAAAATAGTTTATTTTAACTTTCAGAAAGAGATTTCAATGAAA 523
DB 225 AGACATTTCAAGGATCTCTCAGGAAATTCACACCTTGACATTCGATGATGATTTAAAAA 284
QY 524 TTCTAGAGGGTCATGTCAGAAACAATGCTCAAGTATTGTTTATCTACTTTTGCA 582
DB 285 TTCAAAGCGGTCATTTTAAAGTAAGAATAACAGAAATTTAGAAACAAGTATTGAA 343

RESULT 12
BG227279
LOCUS
DEFINITION
kq04903.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5', mRNA
sequence.
ACCESSION
BG227279
VERSION
BG227279.1 GI:12714834
KEYWORDS
EST.
SOURCE
Strongyloides stercoralis
ORGANISM
Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloidea; Strongyloidea.

REFERENCE
1 (bases 1 to 520)
AUTHORS
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

The library was constructed by Dr. Thomas Nutman and colleagues of
NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
High quality sequence stop: 405.

Location/Qualifiers
1. .520
/organism="Strongyloides stercoralis"
/mol_type="mRNA"
/strain="Rhabditiform larvae obtained from gerbils"
/db_xref="taxon:6248"
/lab_host="XL-1 Blue MRF" (Stratagene)"
/clone_lib="TBN95TM-SSR"
/notes="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed

and, using adaptors, was cloned unidirectionally into the
vector from the EcoRI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700)."

ORIGIN

Query Match 2.4%; Score 50.2; DB 2; Length 520;
Best Local Similarity 50.6%; Pred. No. 0.7;
Matches 121; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 344 ATAGTGTGTTTAAGTCGATGCGATTGTCAGATTTTGACGGTAAATTTGAAAAATTTATAGAGCT 403
DB 105 AGATTGATTCATAGAAAATGAATTAGAAGGTGGTGTATTATATAAAAATTTTAGAATA 164
QY 404 ATTATCTTTCTTATCTTGGGCTTGAAGACGGTAAACCCACTTCAAAAGACAAATA 463
DB 165 TAGACAAGTCAAGTAATAGTAATTCAGATTCAGATGTCAGAACAAATAATACAAATG 224
QY 464 ATTCGATATCGCAAAATAGTTTATTTTAACTTTCAGAAAGAGATTTCAATGAAA 523
DB 225 AGACATTTCAAGGATCTCTCAGGAAATTCACACCTTGACATTCGATGATGATTTAAAAA 284
QY 524 TTCTAGAGGGTCATGTCAGAAACAATGCTCAAGTATTGTTTATCTACTTTTGCA 582
DB 285 TTCAAAGCGGTCATTTTAAAGTAAGAATAACAGAAATTTAGAAACAAGTATTGAA 343

RESULT 13
CNS006N9
LOCUS
DEFINITION
CNS006N9 964 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC14J19 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
AL065781
VERSION
AL065781.1 GI:4944661
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 964)
AUTHORS
Genoscope.
Direct Submission

TITLE
JOURNAL
COMMENT
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers
1. 964
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC14J19"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN

Query Match 2.4%; Score 50; DB 10; Length 964;
 Best Local Similarity 30.9%; Pred. No. 0.87; Indels 3; Gaps 2;
 Matches 137; Conservative 108; Mismatches 195;

QY 4 AAAAAGATGAGTCCATATCAATCAAAATATAAATGAATATGAATATGGAATCCTCATCGAAT 63
 DB 521 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 580
 QY 64 AACACAAATACGCAACAGATATCTTTTGGCAATATCGGATATGTCATATGTCAT 123
 DB 581 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 640
 QY 124 TCGAATGATGTCAGGGAATCTCATCGGATGAAT--TTGGGAATCAGTCGAACGATAA 181
 DB 641 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 700
 QY 182 CAAGTATGCGGATAAATCTTATAGAGTTGTGTAGAACCTAGTTTGGGTGGGAATTAATA 241
 DB 701 ADAADAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 760
 QY 242 CACTATATCAATAATAGGAATACTAATCCGACTAATCGTCAAACTGTGTGACGACTTT 301
 DB 761 AADTAKAKWDADKDDKAGAKADKWKAKAAAEAAAWCKDKAKAKAWAAKARWAK 820
 QY 302 CTATATGATGTTATCTATATATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATG 361
 DB 821 AGTGWAARAGAKA-TAGAGAGAKAKAKDKKAGDKADAKADAKADAKADAKADAKADAK 879
 QY 362 CGATTCAGATTTTGGCGGTAATTCGAAATATATAGAGATATATCTTCTTATCTTG 421
 DB 880 AGADKAGAKAKKGGKANAGDAKAKAKAKAKAKAKAKAKAKAKAKAGDDTKDAKARTA 939
 QY 422 GGGCTTGGCTTAAAGACGGTAAA 444
 DB 940 KDAADKAKAKADAKKWKAGWAKA 962

RESULT 14
 BH152435/c
 LOCUS
 DEFINITION
 ENT00777R Entamoeba histolytica Sheared DNA linear GSS 28-AUG-2001
 genomic, genomic survey sequence.

ACCESSION
 BH152435
 VERSION
 BH152435.1 GI:15322563
 KEYWORDS
 GSS.
 ORGANISM
 Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE
 1 (bases 1 to 923)
 Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
 Determination of clone end sequences from Entamoeba histolytica
 HM1:IMSS sheared DNA library (2001)
 Unpublished (2001)
 JOURNAL
 COMMENT
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
 DNA library

Seq primer: M13-Reverse
 Class: shotgun
 High quality sequence start: 18
 High quality sequence stop: 658.
 Location/Qualifiers
 1..923
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HM1:IMSS"
 /db_xref="taxon:5759"

FEATURES
 source

/clone lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHS01; Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v + i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome
 Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Borell, Oxford University Press, 1999)."

ORIGIN

Query Match 2.4%; Score 49.8; DB 9; Length 923;
 Best Local Similarity 45.7%; Pred. No. 0.96;
 Matches 174; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 246 ATTATCAATAATAGGAATACTAATCCGACTAATCGTCAAACTGTGTGACGACTTTCTAT 305
 DB 383 ATAATAAATAAATTCAAACTCTTTTACACATATCTCTGACAGATAATAATAAATAAT 324
 QY 306 ATGTGATTTATTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATCGAT 365
 DB 323 TATTTATTTAATAGTTATATTTTCATCATATTTGAGAGTGAATGTTTCACTTTATTCGTC 264
 QY 366 TCCAGATTTTGGCGGTAATTCGAAATATATAGAGATATATCTTCTTCTTCTTGGGGC 425
 DB 263 ATGATTTATTTCTTGTGAATCATGCTTTTCAACCATCATTAATAATAATAATTTCTTCA 204
 QY 426 TTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAATTCGTATATCGGCAATAGT 485
 DB 203 TAAAGTTGTTATTTAGTTTGAATTTAATGATTTAATAAACTCACCATTCTTTATTTAT 144
 QY 486 TTATTATTTTAAACTTTTCAGAAAGAGATTTCAATGAATTTCTAGAGGGTCAATGTCAG 545
 DB 143 ATTTTATGTTGAATATATCTAATAACAGTTTGATTTGTTTCTTCTTCTTCTTCTTCT 84
 QY 546 AAACAATGCTCAAGTATTTGTTTATTTACCTACTTTTGCACAAGCTGCAAAATGTCAGTTAT 605
 DB 83 ATTCATTATCACTTTTGCTTAATAATACCAGTACATTCAATCAATCAAAATTTATTTAATA 24
 QY 606 ACTATTAAGGATGCGATTCA 626
 DB 23 AATATACATGCTTCCAGCACA 3

RESULT 15
 AZ683446/c
 LOCUS
 DEFINITION
 ENTIR777R Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000
 genomic, genomic survey sequence.

ACCESSION
 AZ683446
 VERSION
 AZ683446.1 GI:11820592
 KEYWORDS
 GSS.
 ORGANISM
 Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE
 1 (bases 1 to 892)
 Loftus, B., Van Aken, S. and Fraser, C.
 Determination of clone end sequences from Entamoeba histolytica
 HM1:IMSS sheared DNA library
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjlloftus@tigr.org
 Clones are derived from the Entamoeba histolytica HM1:IMSS sheared

Seq primer: M13-Reverse
 Class: shotgun
 High quality sequence start: 18
 High quality sequence stop: 658.
 Location/Qualifiers
 1..892
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HM1:IMSS"
 /db_xref="taxon:5759"

Clones are derived from the Entamoeba histolytica HM1:IMSS sheared

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 09:48:39 / Search time 770.097 Seconds
(without alignments)
18018.361 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaaagatggtccata.....acgatctgttaccataaa 2082

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2082	100.0	2082	13 ADR89401	Adt-89401 AXMI-008
2	2082	100.0	5980	13 ADR89400	Adt-89400 AXMI-008
3	2073	99.6	2073	13 ADR89403	Adt-89403 AXMI-008
4	747.2	35.9	2019	13 ADR89414	Adt-89414 AXMI-008
5	747.2	35.9	2145	13 ADR89413	Adt-89413 AXMI-008
6	739.8	35.5	2010	13 ADR89416	Adt-89416 AXMI-008
7	170.2	8.2	1983	3 AAZ93234	Aaz93234 Sequence
8	170.2	8.2	3837	3 AAZ93235	Aaz93235 Sequence
9	168.6	8.1	3471	2 AAX33876	Aax33876 Bacillus
10	168.6	8.1	3471	2 AAX33876	Aax33876 Bacillus
11	160.6	7.7	2407	4 AAS02478	Aas02478 B. thurin
12	102.4	4.9	4366	8 ABX13497	Abx13497 B. popill
13	102.4	4.9	4366	14 AEB90830	Aeb90830 Paenibaci
14	99.6	4.8	1986	13 ADR89411	Adt-89411 AXMI-009
15	99.6	4.8	2019	13 ADR89409	Adt-89409 AXMI-009
16	99.6	4.8	2049	13 ADR89407	Adt-89407 AXMI-009
17	95.6	4.6	3687	4 AAH28240	Aah28240 Nucleotid
18	95.6	4.6	4173	4 AAS02482	Aas02482 B. thurin
19	95.2	4.6	4359	8 ABX13486	Abx13486 B. popill

20	95.2	4.6	4359	14 AEB90814	Aeb90814 Paenibaci
21	94.4	4.5	1959	4 AAS02466	Aas02466 B. thurin
22	93.4	4.5	3684	2 AAV15222	AAV15222 Bacillus
23	93.4	4.5	3684	4 AAB09221	Aab09221 Bacillus
24	93.4	4.5	3684	4 AAS02489	Aas02489 B. thurin
25	93	4.5	1897	3 AAZ33905	AAZ33905 Truncated
26	93	4.5	1897	4 AAH26983	Aah26983 Coding se
27	93	4.5	2019	8 ABV93758	Abv93758 B. thurin
28	93	4.5	2019	8 ABV93759	Abv93759 B. thurin
29	93	4.5	2019	8 ABV93756	Abv93756 Bacillus
30	93	4.5	2019	8 ABV93757	Abv93757 B. thurin
31	93	4.5	3471	2 AAV16516	AAV16516 DNA encod
32	93	4.5	3471	2 AAX83877	Aax83877 Bacillus
33	93	4.5	3471	4 AAS02477	Aas02477 B. thurin
34	93	4.5	3474	4 AAH19323	Aah19323 Cry9C cod
35	93	4.5	4344	2 AAS06782	Aas06782 Insectici
36	93	4.5	4344	2 AAV99986	AAV99986 Nucleotid
37	92.8	4.5	1897	2 AAV13118	AAV13118 Bacillus
38	92.8	4.5	3687	12 ADK98478	Adk98478 B thuring
39	92.8	4.5	3932	2 AAQ64112	Aaq64112 cryET5 ge
40	92.8	4.5	3932	2 AAZ09160	Aaz09160 B. thurin
41	92.8	4.5	3934	2 AAT95051	Aat95051 DNA encod
42	92.8	4.5	3934	2 AAT68434	Aat68434 CryET5 ge
43	92.8	4.5	3934	2 AAV83927	AAV83927 DNA encod
44	92.8	4.5	6930	6 AAD43973	Aad43973 Bacillus
45	92.8	4.5	6930	10 ADF31299	Adf31299 Bacillus

ALIGNMENTS

RESULT 1

ADR89401

ID ADR89401 standard; cDNA; 2082 BP.

XX

AC ADR89401;

XX

DT 18-NOV-2004 (first entry)

XX

DE AXMI-008 coding sequence.

XX

ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
expression cassette; transformation; transgenic; plant; bacteria;
lepidoptera; coleoptera; pest; pesticide; resistance;
pesticidal activity.

OS Bacillus thuringiensis.

XX

FH Key Location/Qualifiers

CDS 1..2082

FT /*tag= a

FT /product= "AXMI-008"

FT /transl_except= pos:1..3, aa:Met

XX WO200407462-A2.

XX 02-SEP-2004..

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782096.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

XX

(ATHE-) ATHENIX CORP.
Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
WPI: 2004-635574/61.
P-PSDB; ADR89402.
New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
and polypeptides, useful for killing lepidopteran or coleopteran pests or
for producing organisms with pesticide resistance.
Claim 1; SEQ ID NO 13; 178pp; English.
This sequence encodes an isolated delta-endotoxin. Some of the delta-
endotoxin coding sequences of the invention have alternative start
codons, producing more than one protein from a single open reading frame.
The nucleic acid sequences of the invention are useful in DNA constructs
or expression cassettes for transformation and expression in plants and
bacteria. The nucleic acids and corresponding polypeptides are useful for
killing lepidopteran or coleopteran pests. Compositions containing the
delta-endotoxins of the invention, and methods for their production, are
useful for the production of organisms with pesticide resistance,
specifically bacteria and plants. These organisms are useful for
generating altered or improved delta-endotoxin or delta-endotoxin-
associated proteins that have pesticidal activity, or for detecting the
presence of delta-endotoxin or delta-endotoxin-associated proteins or
nucleic acids in products or organisms.
Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;
Query Match 100.0%; Score 2082; DB 13; Length 2082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAAAAGATGAGTCCATATCAAAATATAAAATGAATATGAATATTTGGAATCCTCATCG 60
DB 1 GTGAAAAGATGAGTCCATATCAAAATATAAAATGAATATGAATATTTGGAATCCTCATCG 60
QY 61 AATAACACAATAACGGCAACAGATATCCTTTTGGCAATAATCGGGATATGCTACTATG 120
DB 61 AATAACACAATAACGGCAACAGATATCCTTTTGGCAATAATCGGGATATGCTACTATG 120
QY 121 TCTTGGAAATGATGTGAGGGAATCTCATGCGGATGAAATTTGGGAATCAGTCGAAACGATA 180
DB 121 TCTTGGAAATGATGTGAGGGAATCTCATGCGGATGAAATTTGGGAATCAGTCGAAACGATA 180
QY 181 ACAAGTATTCGGGATAAATCTTATAGAGTTTGTATAGAACTAGTTTGGGTGGAATTAAT 240
DB 181 ACAAGTATTCGGGATAAATCTTATAGAGTTTGTATAGAACTAGTTTGGGTGGAATTAAT 240
QY 241 ACATATTAATCAATATAGAAACAACTAAATCCGACTAATCGTCAAACTGTGTGAGCACTT 300
DB 241 ACATATTAATCAATATAGAAACAACTAAATCCGACTAATCGTCAAACTGTGTGAGCACTT 300
QY 301 TCTATATGATTTATATCTATAATTCGTAAGAGAGTAGCCGATAGTGTGTTAAAGTAT 360
DB 301 TCTATATGATTTATATCTATAATTCGTAAGAGAGTAGCCGATAGTGTGTTAAAGTAT 360
QY 361 GCGATTCGAGATTTTCGACGGTAAATTCGAAAATTAATAGAGAGTATTCCTTCTATCTT 420
DB 361 GCGATTCGAGATTTTCGACGGTAAATTCGAAAATTAATAGAGAGTATTCCTTCTATCTT 420
QY 421 GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAA 480
DB 421 GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAA 480
QY 481 TTAGTTTATTTTAAACTTTTCGAAAGAGATTTCAATGAAATTTCTAGAGGGTCATTG 540
DB 481 TTAGTTTATTTTAAACTTTTCGAAAGAGATTTCAATGAAATTTCTAGAGGGTCATTG 540
QY 541 TCAAGAACCAATGCTCAAGTATTTGTTATTAACCTACTTTTCGACAGCTGCAAAATGTGCAG 600
DB 541 TCAAGAACCAATGCTCAAGTATTTGTTATTAACCTACTTTTCGACAGCTGCAAAATGTGCAG 600

QY 601 TTATTTACTATTAAAGGATGCAGTTCAATATATAAAGCAAAATCGTCCCAATTTTGGAGTGA 660
DB 601 TTATTTACTATTAAAGGATGCAGTTCAATATATAAAGCAAAATCGTCCCAATTTTGGAGTGA 660
QY 661 GAGATGTAAAGATCGGAATTAATACCTAACAGTGGTCTGATTTTACCGGTGATTAC 720
DB 661 GAGATGTAAAGATCGGAATTAATACCTAACAGTGGTCTGATTTTACCGGTGATTAC 720
QY 721 TATGAGCGATTAAATATGCAAAACGGCAGATATACCAATTAATTTTATATTTGGTATCAG 780
DB 721 TATGAGCGATTAAATATGCAAAACGGCAGATATACCAATTAATTTTATATTTGGTATCAG 780
QY 781 GTAGTTTAAATTCAGATATAAACAAGGGGGGACAGGTGCTGACACTTGTGTCGAAATTTAAT 840
DB 781 GTAGTTTAAATTCAGATATAAACAAGGGGGGACAGGTGCTGACACTTGTGTCGAAATTTAAT 840
QY 841 AAATTTCTAGAGAAATGACGTTGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTAT 900
DB 841 AAATTTCTAGAGAAATGACGTTGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTAT 900
QY 901 GATTTTGAGAAATATCCATTGCGCAACATGCTAGAGTTGACTAGGGAAATTTATACAGAT 960
DB 901 GATTTTGAGAAATATCCATTGCGCAACATGCTAGAGTTGACTAGGGAAATTTATACAGAT 960
QY 961 GCAGTGGGATATTCATTCGGGAACTTATATAGTTGGTTACGGAATTTGGCCTTAATCTTTTAA 1020
DB 961 GCAGTGGGATATTCATTCGGGAACTTATATAGTTGGTTACGGAATTTGGCCTTAATCTTTTAA 1020
QY 1021 GGGTTAGAGGCTTAATGGAAACACGGGGACCTGGTTTGTAGTTTACCTGGCTTAGCAAAATAGT 1080
DB 1021 GGGTTAGAGGCTTAATGGAAACACGGGGACCTGGTTTGTAGTTTACCTGGCTTAGCAAAATAGT 1080
QY 1081 ATATATAATAGTATGTTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGCTATTATGAA 1140
DB 1081 ATATATAATAGTATGTTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGCTATTATGAA 1140
QY 1141 GACTACACAAAGGGTAAACGGTATTTTCAAGTATGCTGGAACCTACGAGTAATGATCTA 1200
DB 1141 GACTACACAAAGGGTAAACGGTATTTTCAAGTATGCTGGAACCTACGAGTAATGATCTA 1200
QY 1201 CGTATATTTGATTTTTCAGAACTCCGATGATATAAAATTTACTTCAATTTAGCTATCATGAC 1260
DB 1201 CGTATATTTGATTTTTCAGAACTCCGATGATATAAAATTTACTTCAATTTAGCTATCATGAC 1260
QY 1261 CTAGTAGAGAGACTACCGCTAGACAGAGTATCGTGTTCGAGGAGATTTTTCGTAGG 1320
DB 1261 CTAGTAGAGAGACTACCGCTAGACAGAGTATCGTGTTCGAGGAGATTTTTCGTAGG 1320
QY 1321 GTAGGGGACCTGATTTTAAATTAATGATGCGAGTAATTAATGGGCTTAAGCAGGATGCAAT 1380
DB 1321 GTAGGGGACCTGATTTTAAATTAATGATGCGAGTAATTAATGGGCTTAAGCAGGATGCAAT 1380
QY 1381 GAATCTAGTTCCTCCACTTGTATTTGACCTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440
DB 1381 GAATCTAGTTCCTCCACTTGTATTTGACCTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440
QY 1441 TCAAAATGGCGCATGTGTTGATATATGGAATCTCCAGAGTTAAACGATATATGTTTGGACAT 1500
DB 1441 TCAAAATGGCGCATGTGTTGATATATGGAATCTCCAGAGTTAAACGATATATGTTTGGACAT 1500
QY 1501 ACAAGTTTAAACCGTGAATAATAATTAAGAGCAATCAAAATTAACAAATACCGGGGTG 1560
DB 1501 ACAAGTTTAAACCGTGAATAATAATTAAGAGCAATCAAAATTAACAAATACCGGGGTG 1560
QY 1561 AAGAGTTTAACTTCAAAATTTATCTGCTAATGCTATACCTATGTAATAAAGCACT 1620
DB 1561 AAGAGTTTAACTTCAAAATTTATCTGCTAATGCTATACCTATGTAATAAAGCACT 1620
QY 1621 CATACAGGTGGGGATTTAATCCGTTTAAAGAAACAAATCAGAGTATAACCGAGTTTAT 1680
DB 1621 CATACAGGTGGGGATTTAATCCGTTTAAAGAAACAAATCAGAGTATAACCGAGTTTAT 1680

QY 1681 GCAGTGGCGGAATTAGATTGATTATTAATAACAAACCTGCAGACAAAGTTACCGTATT 1740
DB |||||||
1681 GCAGTGGCGGAATTAGATTGATTATTAATAACAAACCTGCAGACAAAGTTACCGTATT 1740
QY 1741 CGTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTAGTGATATCTTTATCCAGGAGGT 1800
DB |||||||
1741 CGTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTAGTGATATCTTTATCCAGGAGGT 1800
QY 1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAAAAATCTTACTCTGGAATTTATGACGATTTA 1860
DB |||||||
1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAAAAATCTTACTCTGGAATTTATGACGATTTA 1860
QY 1861 AAATATAGTGAATTTAAATTCGCTGAAATATATCAACCTCCATPACCTAGTCTCAAAACATT 1920
DB |||||||
1861 AAATATAGTGAATTTAAATTCGCTGAAATATATCAACCTCCATPACCTAGTCTCAAAACATT 1920
QY 1921 CAGATGATGCGGATGCAAGCGAATAGTTTCAATCAGATGTAACGTTGGTCTCGAC 1980
DB |||||||
1921 CAGATGATGCGGATGCAAGCGAATAGTTTCAATCAGATGTAACGTTGGTCTCGAC 1980
QY 1981 AAAATTGAAATTCCTCCCAAGTAATACAACTTTAGAAATAGAGGAGAACGGACCTA 2040
DB |||||||
1981 AAAATTGAAATTCCTCCCAAGTAATACAACTTTAGAAATAGAGGAGAACGGACCTA 2040
QY 2041 GAAAAACAAAGAACGCGGTGAACGATCTGTTTACCAATTA 2082
DB |||||||
2041 GAAAAACAAAGAACGCGGTGAACGATCTGTTTACCAATTA 2082

RESULT 2

ADR89400
ID ADR89400 standard; cDNA; 5980 BP.
AC ADR89400;
XX
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 full length coding sequence.
XX
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.

Key	Location/Qualifiers
FT CDS	168..2249
FT	/*tag= a
FT	/product= "AXMI-008"
FT	/transl_except= pos:168..170, aa:Met

WO2004074462-A2.

XX
XX
PD 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.

PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89402.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 12; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.

XX Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;

Query Match 100.0%; Score 2082; DB 13; Length 5980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTGAAAAGATGATGCTCATATCAAAATAAATGAATATGAATATGGATCTCATCG	60
DB	168	GTGAAAAGATGATGCTCATATCAAAATAAATGAATATGAATATGGATCTCATCG	227
QY	61	AATAACACAAATACGCCAACAGATATCCTTTTGCAATAAATCGGATATGTCTACTATG	120
DB	228	AATAACACAAATACGCCAACAGATATCCTTTTGCAATAAATCGGATATGTCTACTATG	287
QY	121	TCTTGGAAATGATGTTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA	180
DB	288	TCTTGGAAATGATGTTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA	347
QY	181	ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGTGAATTAAT	240
DB	348	ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGTGAATTAAT	407
QY	241	ACACTATTATCAATAATAGCAAACTAAATTCGACTAAATCGTCAAACTGTGTGAGCACTT	300
DB	408	ACACTATTATCAATAATAGCAAACTAAATTCGACTAAATCGTCAAACTGTGTGAGCACTT	467
QY	301	TCTATATGATTTATTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTAAAGTGAT	360
DB	468	TCTATATGATTTATTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTAAAGTGAT	527
QY	361	GGGATTGCAGATTTTCACCGTAAATTTGAAAATTTATAGAGATTTATCTTTCTTATCTT	420
DB	528	GGGATTGCAGATTTTCACCGTAAATTTGAAAATTTATAGAGATTTATCTTTCTTATCTT	587
QY	421	GGGGCTTGGCTTAAAGACCGGTAAACCACTTTCAAAACAAATAATTTCTGATATCGGACAA	480
DB	588	GGGGCTTGGCTTAAAGACCGGTAAACCACTTTCAAAACAAATAATTTCTGATATCGGACAA	647
QY	481	TTAGTTTATTTATTTTAACTTTTCAGAAAGAGATTTTCAATGAAATTTCTAGGAGGTCATTG	540
DB	648	TTAGTTTATTTATTTTAACTTTTCAGAAAGAGATTTTCAATGAAATTTCTAGGAGGTCATTG	707
QY	541	TCAAGAAACAATGCTCAAGTATTTGTTATACCTACTTTTGGCAACAGCTGCAATGTGCAG	600
DB	708	TCAAGAAACAATGCTCAAGTATTTGTTATACCTACTTTTGGCAACAGCTGCAATGTGCAG	767
QY	601	TTATTACTATTAAAGGATGCAGTTTCAATATATAAGCAACAATGGTTCCCATTTTTTGAGTGCA	660

Db 768 TTTATTACTATTAGGGATGCAATTAATATAAGCAATGGTTCCCATTTTGGAGTGA 827
Qy 661 GAGAAATGTAAGATCGGAATTAATATACCTAACAGTGGTTGTGATTTTACCGGTGATTAC 720
Db 828 GAGAAATGTAAGATCGGAATTAATATACCTAACAGTGGTTGTGATTTTACCGGTGATTAC 887
Qy 721 TATAGCGATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATATGTTGATACAG 780
Db 888 TATAGCGATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATATGTTGATACAG 947
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTGGAAATTTAAT 840
Db 948 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTGGAAATTTAAT 1007
Qy 841 AAATTTTCGTAGAAAATGACGTTGGCGGTATTGCGATATTATCGCTATATTTCNAACTTAT 900
Db 1008 AAATTTTCGTAGAAAATGACGTTGGCGGTATTGCGATATTATCGCTATATTTCNAACTTAT 1067
Qy 901 GATTTTGGAGAAATATCCATTGCGCAACACATGTAAGTGTGACTAGGAGAAATTTATACAGAT 960
Db 1068 GATTTTGGAGAAATATCCATTGCGCAACACATGTAAGTGTGACTAGGAGAAATTTATACAGAT 1127
Qy 961 GCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGNAATGGCCTAATACTTTTAAT 1020
Db 1128 GCAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGNAATGGCCTAATACTTTTAAT 1187
Qy 1021 GCGTTAGAGGCTAATGGAAACACGGGACCTGGTTTGTAGTTTACTTTGGCTTAGCAAAATAGGT 1080
Db 1188 GCGTTAGAGGCTAATGGAAACACGGGACCTGGTTTGTAGTTTACTTTGGCTTAGCAAAATAGGT 1247
Qy 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCAATATGAA 1140
Db 1248 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCAATATGAA 1307
Qy 1141 GACTACACAAGGGTAACGGTATTTTCAACGTATGCTGGAACTACGAGTATGATCTA 1200
Db 1308 GACTACACAAGGGTAACGGTATTTTCAACGTATGCTGGAACTACGAGTATGATCTA 1367
Qy 1201 CGTAATATTGATTTTCAGAAATGCGATGTATATAAAATTTACTTTCATTAGCTATCATGAAC 1260
Db 1368 CGTAATATTGATTTTCAGAAATGCGATGTATATAAAATTTACTTTCATTAGCTATCATGAAC 1427
Qy 1261 CTAGTAGGAGAGACTACCGCTAGACCAAGATATCGTGTTCAAAGGCAGATTTTCGTAGG 1320
Db 1428 CTAGTAGGAGAGACTACCGCTAGACCAAGATATCGTGTTCAAAGGCAGATTTTCGTAGG 1487
Qy 1321 GTAGGGGGACCTGATTTAAATTTATGATGACAGTAAATAATGCGCTTAAGCAGGATGACAAAT 1380
Db 1488 GTAGGGGGACCTGATTTAAATTTATGATGACAGTAAATAATGCGCTTAAGCAGGATGACAAAT 1547
Qy 1381 GAATCTACGTTCCCACTTGTATTGCACTCTAATGCGTGTAGAGGACCTCTCATAGATTA 1440
Db 1548 GAATCTACGTTCCCACTTGTATTGCACTCTAATGCGTGTAGAGGACCTCTCATAGATTA 1607
Qy 1441 TCAAAATCGGCATGTGTGTATATGGAACCTCCAGAGTTAACGTATATGTTTGGACACAT 1500
Db 1608 TCAAAATCGGCATGTGTGTATATGGAACCTCCAGAGTTAACGTATATGTTTGGACACAT 1667
Qy 1501 ACAAGTTTAAACGTAAGAAATATAATTTGAAGCCCAATCAAAATTTACAAAATACCGCGGTG 1560
Db 1668 ACAAGTTTAAACGTAAGAAATATAATTTGAAGCCCAATCAAAATTTACAAAATACCGCGGTG 1727
Qy 1561 AAGAGTTTATTTACCTTCAAAATTTATCTTGTCTAATGCGCTATACCTATGTAAATAAAGGCAC 1620
Db 1728 AAGAGTTTATTTACCTTCAAAATTTATCTTGTCTAATGCGCTATACCTATGTAAATAAAGGCAC 1787
Qy 1621 CATACAGGTGGGATTTAATCCGTTTTTAAAGACAAAATCAGAGTATAACGCGATTTAT 1680
Db 1788 CATACAGGTGGGATTTAATCCGTTTTTAAAGACAAAATCAGAGTATAACGCGATTTAT 1847
Qy 1681 GCAGGTGGCGGAATTTAGATTTGATTTAATAACAAAATCTCAGGACAAAATGTTACCGTATT 1740

Db 1848 GCAGGTGGCGGAATTTAGATTTGATTTAATAACAAAATCTCAGGACAAAATGTTACCGTATT 1907
Qy 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTTAGTGATATATCTTTATCCAGAGGT 1800
Db 1908 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTTAGTGATATATCTTTATCCAGAGGT 1967
Qy 1801 TGGGGTTCAAATCGTTTGTATCGCTTGAAAATCTTACTCTGGAATATATGACGATTTA 1860
Db 1968 TGGGGTTCAAATCGTTTGTATCGCTTGAAAATCTTACTCTGGAATATATGACGATTTA 2027
Qy 1861 AAATATAGTGAATTTTAAATTCGCTGAAATTTACACCTCCATTAACCTAGTTCAAAATTT 1920
Db 2028 AAATATAGTGAATTTTAAATTCGCTGAAATTTACACCTCCATTAACCTAGTTCAAAATTT 2087
Qy 1921 CAGATGGATGTGAGATCGAATGATGTTTCAATCAGATGTTAAACGTTCTCGAC 1980
Db 2088 CAGATGGATGTGAGATCGAATGATGTTTCAATCAGATGTTAAACGTTCTCGAC 2147
Qy 1981 AAATTTGAATTCCTCCCAAGTAATACAACTTTTAGAATATGAGGAGAACGGGACCTA 2040
Db 2148 AAATTTGAATTCCTCCCAAGTAATACAACTTTTAGAATATGAGGAGAACGGGACCTA 2207
Qy 2041 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTA 2082
Db 2208 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTA 2249
RESULT 3
ADR89403
ID ADR89403 standard; cdna; 2073 BP.
XX
AC ADR89403;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 alternative start site coding sequence.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
OS Bacillus thuringiensis.
XX
FH Key
CDS 1. .2073
FT /*tag= a
FT /product= "Alternative AXMI-008"
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PP 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR

DR P-PSDB; ADR89404.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 15; 178pp; English.

CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.

XX Sequence 2073 BP; 694 A; 305 C; 431 G; 643 T; 0 U; 0 Other;

Query Match 99.6%; Score 2073; DB 13; Length 2073;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGAGTCCATCAAAATAAAATGAATGAATATGAATATGGAATCCTCATCGAATAACACA 69
 DB 1 ATGAGTCCATCAAAATAAAATGAATGAATATGGAATCCTCATCGAATAACACA 60

QY 70 AATACGCCAACAGATATCTTTTGCNAATAATCGGGATATGCTACTATGCTTGGAAAT 129
 DB 61 AATACGCCAACAGATATCTTTTGCNAATAATCGGGATATGCTACTATGCTTGGAAAT 120

QY 130 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 189
 DB 121 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 180

QY 190 GGGATAAATCTTATAGAGTTTGTATAGAACCTAGTTTGGGTGGAATTAATACACTATTA 249
 DB 181 GGGATAAATCTTATAGAGTTTGTATAGAACCTAGTTTGGGTGGAATTAATACACTATTA 240

QY 250 TCAATAATAGGAACCTAATTCGACTAATCGTCAAACTGTGTCAGCACTTCTATATGT 309
 DB 241 TCAATAATAGGAACCTAATTCGACTAATCGTCAAACTGTGTCAGCACTTCTATATGT 300

QY 310 GATTATATCTATATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATGCGATTGCA 369
 DB 301 GATTATATCTATATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATGCGATTGCA 360

QY 370 GATTTTGACGGTAAATTTGAAAAATATAGAGAGTATTATCTTTCTTATCTTGGGGCTTGG 429
 DB 361 GATTTTGACGGTAAATTTGAAAAATATAGAGAGTATTATCTTTCTTATCTTGGGGCTTGG 420

QY 430 CTTAAAGACGGTAAACCACTTCAAAAGACAAATTTCTGATATCGGCAATTAGTTTAT 489
 DB 421 CTTAAAGACGGTAAACCACTTCAAAAGACAAATTTCTGATATCGGCAATTAGTTTAT 480

QY 490 TATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCATTTGTCAGAAAC 549
 DB 481 TATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCATTTGTCAGAAAC 540

QY 550 AATGCTCAAGTATGTTATTAACCTACTTTTGGCAAGAGCTGCAATGTCAGTTTATTA 609
 DB 541 AATGCTCAAGTATGTTATTAACCTACTTTTGGCAAGAGCTGCAATGTCAGTTTATTA 600

QY 610 TTAAGGATGACAGTTCAATATAAAGCAATGTTCCCATTTTGTAGTGACAGAAATGTA 669
 DB 601 TTAAGGATGACAGTTCAATATAAAGCAATGTTCCCATTTTGTAGTGACAGAAATGTA 660

QY 670 AGATCGGAATTAATATACACCTAACAGTGGTGTGATTTTACCGGTGATTACTATGACGGA 729
 DB 661 AGATCGGAATTAATATACACCTAACAGTGGTGTGATTTTACCGGTGATTACTATGACGGA 720

QY 730 TTAATAATGCAAAACGGCAGAGTATACCAATTTATTTGTTATTTGGTATCAGGTAGGTTTA 789
 DB 721 TTAATAATGCAAAACGGCAGAGTATACCAATTTATTTGTTATTTGGTATCAGGTAGGTTTA 780

QY 790 AATCAGATTAACACAGGGGGGACAGTGTGACACTTGTGCAAAATTTAATAAATTCGT 849
 DB 781 AATCAGATTAACACAGGGGGGACAGTGTGACACTTGTGCAAAATTTAATAAATTCGT 840

QY 850 AGAATAATGACGTTGCGGGTATTGGATATTATCGCTATATTTCCTCACTATGATTTTGGAG 909
 DB 841 AGAATAATGACGTTGCGGGTATTGGATATTATCGCTATATTTCCTCACTATGATTTTGGAG 900

QY 910 AATATCCATTTGCGCAACACATGTPAGTGTGACTAGGGAAATTTTATACAGATGCGATGGGA 969
 DB 901 AATATCCATTTGCGCAACACATGTPAGTGTGACTAGGGAAATTTTATACAGATGCGATGGGA 960

QY 970 TATTCATCGGGAATCTTATAGTTGGTTACGGAATTTGCGCTTAATCTTTTAAATGGGTAGAG 1029
 DB 961 TATTCATCGGGAATCTTATAGTTGGTTACGGAATTTGCGCTTAATCTTTTAAATGGGTAGAG 1020

QY 1030 GCTAATGGAACACGGGGACCTGGTTTGTAGTTTACTTTGGCTTAGCAAAATAGGTATATAAT 1089
 DB 1021 GCTAATGGAACACGGGGACCTGGTTTGTAGTTTACTTTGGCTTAGCAAAATAGGTATATAAT 1080

QY 1090 GAGTATGTTTCGAGATATTATTTGCCGGCTGGGTAGGAACTCGTCATTTATGAAGACTACACA 1149
 DB 1081 GAGTATGTTTCGAGATATTATTTGCCGGCTGGGTAGGAACTCGTCATTTATGAAGACTACACA 1140

QY 1150 AAGGGTAAACGGTATTTTCAACGATGCTCGGAACTACGAGTAATGATCTACGTAATATT 1209
 DB 1141 AAGGGTAAACGGTATTTTCAACGATGCTCGGAACTACGAGTAATGATCTACGTAATATT 1200

QY 1210 GATTTTCAGAAATGCCGATGATATAAAATTTACTTTCATTTAGCTATCATGAACCTAGTAGGA 1269
 DB 1201 GATTTTCAGAAATGCCGATGATATAAAATTTACTTTCATTTAGCTATCATGAACCTAGTAGGA 1260

QY 1270 GAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGCAGATTTTCGTAGGGTAGGGGGA 1329
 DB 1261 GAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGCAGATTTTCGTAGGGTAGGGGGA 1320

QY 1330 CCTGATTTAAATTTATGATCGAGTAATTAATGGCTTAAGCAGAGTGAATTTGAATCTACG 1389
 DB 1321 CCTGATTTAAATTTATGATCGAGTAATTAATGGCTTAAGCAGAGTGAATTTGAATCTACG 1380

QY 1390 TTCCCACTTTGATTTGACCTCTAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCG 1449
 DB 1381 TTCCCACTTTGATTTGACCTCTAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCG 1440

QY 1450 GCATGTTGTTGATATGGAACCTCCAGAGTTAAACGATATATGTTTGGACACATACAAGTTTA 1509
 DB 1441 GCATGTTGTTGATATGGAACCTCCAGAGTTAAACGATATATGTTTGGACACATACAAGTTTA 1500

QY 1510 AAAAGTGAATAATTAATTTGAAGCAATCAAAATTAACAATAACCGGCGGTGAAGATTAT 1569
 DB 1501 AAAAGTGAATAATTAATTTGAAGCAATCAAAATTAACAATAACCGGCGGTGAAGATTAT 1560

QY 1570 TACCTTCAAAATTTATCTTCTGCTAATGCTATACCTATGTAATAAAGGCCACTCATACAGGT 1629
 DB 1561 TACCTTCAAAATTTATCTTCTGCTAATGCTATACCTATGTAATAAAGGCCACTCATACAGGT 1620

QY 1630 GGGGATTTAATCCGTTTTTTTAAAGAACAAATCAGAGTATAACCGAGTTTATGTCAGGTGGC 1689
 DB 1621 GGGGATTTAATCCGTTTTTTTAAAGAACAAATCAGAGTATAACCGAGTTTATGTCAGGTGGC 1680

QY 1690 GGAATTAGATTGATTTAATAAACAACCTGACAGCAAAAGTTACCGTATTCGTTTTCGT 1749
 DB 1681 GGAATTAGATTGATTTAATAAACAACCTGACAGCAAAAGTTACCGTATTCGTTTTCGT 1740

QY 1750 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTTATCCAGGAGGTTGGGTTCA 1809

Db 1741 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGATATCTTTATCCAGAGGTTGGGGTTCA 1800
QY 1810 AATCGGTTTTGTATCGCTTGAAAATCTTACTCTGGAAATTAATGACGATTTAAATATAGT 1869
Db 1801 AATCGTTTTGTATCGCTTGAAAATCTTACTCTGGAAATTAATGACGATTTAAATATAGT 1860
QY 1870 GATTTTAAATTCGCTGAAATATACACCTCCATTAACCTAGTTTCAACATTCAGATGGAT 1929
Db 1861 GATTTTAAATTCGCTGAAATATACACCTCCATTAACCTAGTTTCAACATTCAGATGGAT 1920
QY 1930 GTGAGATCAACCGAATAGTTTTCATCAGATGTAAACCTGCTTCGCACAAAATTGAA 1989
Db 1921 GTGAGATCAACCGAATAGTTTTCATCAGATGTAAACCTGCTTCGCACAAAATTGAA 1980
QY 1990 TTCTCTCCCAAGTAATACAACTTTAGAAATATGAGGAGAACGGGACCTAGAAAAAACA 2049
Db 1981 TTCTCTCCCAAGTAATACAACTTTAGAAATATGAGGAGAACGGGACCTAGAAAAAACA 2040
QY 2050 AGAAGCGGTGAACGATCTGTTTACCAATTAA 2082
Db 2041 AAGAAGCGGTGAACGATCTGTTTACCAATTAA 2073

RESULT 4
ADR89414
ID ADR89414 standard; cDNA; 2019 BP.
XX
AC ADR89414;
XX
DT 18-NOV-2004 (first entry)
XX
DE AXMI-008 coding sequence.
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 1..2019
FT /*tag= a
FT /product= "AXMI-008"
FT /transl_except= pos:1.. .3, aa:Met
XX
PN WO2004074462-A2.
XX
PD 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
PA (ATHE-) ATHENIX CORP.
XX
PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX
DR WPI; 2004-635574/61.
DR P-PSDB; ADR89415.
XX

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 26; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;
Query Match 35.9%; Score 747.2; DB 13; Length 2019;
Best Local Similarity 69.8%; Pred. No. 9.9e-160; Indels 72; Gaps 7;
Matches 1143; Conservative 0; Mismatches 423;
QY 1 GTGAAAAAGATGAGTCCATATCAAAATATAATGAATATGAATATTTGGAATCTTCATCG 60
Db 1 GTGAAAAATATGAATCTTATCAAAATACAATGAATGAATTTCTGGATGTTCCCG 60
QY 61 AATAACACAAATACGCCAAAACAGATATCTTTTGAATATATCGGGATATGTCTACTATG 120
Db 61 AATAACACAAATATGTCAACAGATATCTTTTGAAGAGATCAAAATATATTTCTAT 120
QY 121 TCTTGAATGATTGTTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA 180
Db 121 AACCTGGACGCTTGTACGGGAAGGCCATGGAAGATACGTGGGAATCAGTCTCGGATATA 180
QY 181 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240
Db 181 GTAACCTATTTGGGACATACCTTATACAATCTTTGTAGAACCCGGTATAGTGGAAATTCCT 240
QY 241 ACATATATCAATATAGGAAAACATAATCCGACTAATCGTCAAACTGTGTGAGCAGCTT 300
Db 241 GTAATATTTCAATAATAAACAACACTCATTCGCTCTTCGTGCAATCTGTGGCAGCAGCTT 300
QY 301 TCTATATGTGATTTTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGAT 360
Db 301 TCTATATGTGATTTAGTATCTATATATTCGTAAGAGGTAGACGAGCGGTGTTAAGTGAC 360
QY 361 GCGATTTGCAGATTTTGGCGTAAATTTGAAAAATATAGAGATATATCTTTCTTATCTT 420
Db 361 GGGGTTGCAGATTTTGGGGTGAATGACTGCTTATCAAGATTAATATCTTCATTTATCTT 420
QY 421 GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTCATATCGACAA 480
Db 421 GAGGATTTGGCTTACAG-----ATNAATCAAAATCCTTAAAAAATCTGCTGAC 465
QY 481 TTAGTTTATATTTTAAACTTTTTCAGAAAGAGATTTCAATGAAATCTTAGGAGGTCATTTG 540
Db 466 GTAGTTTAAAGTTTCAAGCACGGGAAGAGATTTTCACTAACTTTTAGCAGGGTCATTTA 525
QY 541 TCAAGAAACAATGCTCAAGTATTTGTTATTA CTTACTTTTGGCA CAGCTCAAAATGTGCAG 600
Db 526 TCAAGACAGAAAGCTGAAATATTAATTTGCTCTACGTATGTGCAAGCTGCAAAATGTGCAT 585
QY 601 TTATTACTATTAAAGGATCGAGTCAATATATAAGCACATGTTCCCATTTTGTAGTGCA 660
Db 586 TTATTACTATTAAAGGACCGCAGTTAAATATAAAAAAGAAATGGGACCTAGTGTGTCACCG 645
QY 661 GAGNAATGTAAGATCGGAATTAATATCACCTAACAGTGGTGTGTGATTTTCCCGTGATTAC 720

Db 646 TTGTATCCAGGGTCAAGGAGAA-----CTGATTGT 675
Qy 721 TATCAGCGATTAAATCAAAACGCGAGAGTATACCAATTATTTGTTTATATTTGTTATCAG 780
Db 676 AACAGCGGTTAAAGCGAAATAAAGAGTATCTAATTATTTGTTAGGGTGGTATAAC 735
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTCTGACACTTGGTTCGAAATTTAAT 840
Db 736 AAGGGTTTAGATCAGATAAGACAGCGGGTACAAGTCTGAAGTTTGGTTCGAAATTTAAT 795
Qy 841 AATTTTCGTAGAGAAATCAGTTGGCGGTATTTGATATATTCGCTATATTTCCAACTTAT 900
Db 796 AATTTTCGTAGAGAAATGAGCTTGGCGGTATTTGATATATTTGCTATATTTCCAACTTAT 855
Qy 901 GATTTTCAGAGAAATCCATTCGCAACACATGTAGAGTTGACTAGGGAAATTTTACAGAT 960
Db 856 GATTTTCAGAGAAATCCATTTAGCAACAAGTGTAGAGTTAATAGGGAAATTTTACAGAT 915
Qy 961 GCAGTGGGATATTCATCGGGAATTTATGTTGGTTACGGAATTTGGCTTAATCTTTTAAAT 1020
Db 916 CCAGTGGGATATTCAGGGGGAATTTATGTTGGGAACGGTTT-----TTAGCTTTAAT 969
Qy 1021 GGGTTAGAGCTAATGCAACCGGGACCTGGTTTACTTGGCTTGGCTTACCAAAATAGGT 1080
Db 970 TCGGTAGAGCAAAATGGAACACGGGGACCTGGTTTACTTGGCTTCAAGCTATAGAT 1029
Qy 1081 ATATATATGATGATGTT-----TCGAGATATTTTCGCGCTGGGTAGGAACCTCGT 1131
Db 1030 ATATATAGTCACTTATTAATCTTCAGCTTGGTTTATCTTAGTGGCTGGGGGGAACCTCGT 1089
Qy 1132 CATTATGAAGACTACACAAAGGGTAAACGGTATTTTTCACGCTATGCTCGGAACCTACGAGT 1191
Db 1090 CATTATGAAGACTTACAAAGGGTAAACGGTGTCTTTCACGCTATGCTCGGAACCTACGAGT 1149
Qy 1192 AATGATCTAGTAAATATGATTTTTCAGATGCGGATGATATAAATAATCTTCAATAGCT 1251
Db 1150 AATAATCCAGTAAATATTTATTTTGGCAATACCGATATATTTAAATAATTTTCAATAGCT 1209
Qy 1252 A---TCATGAACCTAGTAGGAGAGACTACCGCTAGACGAGTATCGTGTTCAAAGGCA 1308
Db 1210 AGATATGCAATGCAACCGTTTGGTGTATTCATCCCGGCATCTGTTTCACTGCA 1269
Qy 1309 GATTTTCGTAGGTAGGGGACCTGATTTTAAATATATGATGCAAGTAAATATGGGCTAAGC 1368
Db 1270 GAATTTTTCGACACACACTAAATCTTCTGTATGAGGTAAACAGTCTCGG---TAC 1326
Qy 1369 AGGATGCAATGAAATCTAGCTCCCACTTGT-----ATTGCACTCTAATGTTGTAGA 1422
Db 1327 TCACAGACAATGAAATCTGTGTACCAGGTATTAATAAGGATCTACCACCTAGTCGTACA 1386
Qy 1423 GGACCTCTCATAGATTATCAAAATGCGCATGTTGTATATGGAACCTCCAGATTAC 1482
Db 1387 AATTACTCTCATAGATTATCAAAATGCGCATGTTGTCAAAATGAAACCTCCAGATTAC 1446
Qy 1483 GTATATGTTTGGACACATACAAGTTTAAACGTTGAAATATATAATGAAGCAATCAAAAT 1542
Db 1447 GTATTTGTTGGACACATACAAGTATGAAABAGATATCGAATTTATCCAGATAAAT 1506
Qy 1543 ACACAAATCCGGGGTGAAGAGTTATTAATCTTCAAAATTAATCTTGAATGCTATACC 1602
Db 1507 ACGCAAAATCTTCAGTAAAGCTTTTGGCCCTACCAGCAGGTACAGGATATCGAGGAGT 1566
Qy 1603 TATGTAATAAAGGCACT 1620
Db 1567 TACGTACACGCTGGGCT 1584

RESULT 5
ADR89413
ID ADR89413 standard; cDNA; 2145 BP.
XX
AC ADR89413;
XX

DT 18-NOV-2004 (first entry)
XX AXMI-008 full length coding sequence.
DE
XX
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 127..2145
FT /*tag= a
FT /product= "AXMI-008"
XX /transl_except= pos:127..129, aa:Met
PN WO2004074462-A2.
XX
XX 02-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005829.
XX
PR 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-044879P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-0078197P.
PR 19-FEB-2004; 2004US-0078202P.
PR 19-FEB-2004; 2004US-0078209P.
PR 19-FEB-2004; 2004US-0078214P.
PR 19-FEB-2004; 2004US-0078257P.
PR 19-FEB-2004; 2004US-0078341P.
XX
XX (ATHE-) ATHENIX CORP.
XX
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89415.
XX
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
PS Claim 1; SEQ ID NO 25; 178pp; English.
XX
CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
SQ Sequence 2145 BP; 710 A; 338 C; 441 G; 656 T; 0 U; 0 Other;
XX
Query Match 35.9%; Score 747.2; DB 13; Length 2145;
Best Local Similarity 69.8%; Pred. No. 18-159;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;
Qy 1 GTGAAAAGATGAGTCCATATCAAAATAAAAATGAATATGAATATTTGGAATCTCATCG 60
Db 127 GTGAAAATATGAATCTTATCAAAATACAAATGAATGAATATTTGATGTTCCCG 186

QY	61	ATAACACAAATACGCCAAACAGATATCCTTTTGC	120
DB	187	ATAACACAAATATGTCAACAGATATCCTTTTGC	246
QY	121	TCCTGGAATGATTTGTCAGGGAATCTCATGGGAT	180
DB	247	AACCTGGAGCTTTGTCAGGGAAGGCCATGGCAAG	306
QY	181	ACAAGTATTTGGGATAAATCTTATAGAGTTTGT	240
DB	307	GTAACCTATTTGGGACATACCTTATACAATCTT	366
QY	241	ACACTATTAATCAATATAGGAAACCTAAATTCG	300
DB	367	GTAATATTTTCAATATAAACCAAACTCATTCCT	426
QY	301	TCATATGATGATTTATTAATCTATAATTCGTAAG	360
DB	427	TCATATGATGATTTAGTATCTATAATTCGTAAGG	486
QY	361	GCGATTTGCAGATTTTGACCGGTAAATTTGAAA	420
DB	487	GCGGTTTGCAGATTTTGGGGTGAATATGACTGT	546
QY	421	GCGGCTTGGCTTAAAGACGGTAAACCACTTTCA	480
DB	547	GAGGATTTGGCTTACAG-----ATAAATCAATC	591
QY	481	TTAGTTTATTAATTTTAAACTTTTCAGAAAGAGA	540
DB	592	GTAAGTAAACAGTTCCAAGCACGGGAAGAAGAT	651
QY	541	TCAGAAACCAATGCTCAAGTATGTTATTAACCT	600
DB	652	TCAAGACAGAAAGCTGAAATATTAATTTAGCCT	711
QY	601	TTATTAATTAAGGATGCAGTTCAATATAAAGCAC	660
DB	712	TTATTAATTAAGGGACCGAGTTAAATATAAABA	771
QY	661	GAGAAATGAAGATCGGAATTAATATCACTAACG	720
DB	772	TTGTATCCAGGGTCAGGGAGAA-----CTGAT	801
QY	721	TATGACGGATTAATAATGCAAAACCGCAGAGTA	780
DB	802	AACGACGGTAAAGCGGAAATAAAGAGTATATCA	861
QY	781	GTAAGTTTAAATCAGATATAAACAGGGGGGACA	840
DB	862	AAGGTTTATAGATCAGATAGACAGGCGGGTACA	921
QY	841	AAATTTTCGTAGAAATGACGTTGGCGGTATTCG	900
DB	922	AAATTTTCGTAGAAATGACGTTGGCGGTATTCG	981
QY	901	GATTTTTCGAGAAATATCCATTTGCCAACACAT	960
DB	982	GATTTTGAATAATATCCATTAAGCAACAGTGTAG	1041
QY	961	CGAGTGGGATTTTCATCGGGAACTTATAGTTGG	1020
DB	1042	CCAGTGGGATTTTCAGGGGGAATTTATGGTTGG	1095
QY	1021	GGGTTAGAGCTTAATGGAACACCGGGACCTGGT	1080
DB	1096	TCGGTAGAGCAAAATGGAACACCGGGACCTGGT	1155
QY	1081	ATATATAATGAGTATGTT-----TCGAGATAT	1131
DB	1156	ATATATAGTCATTTCTATTAATCTTCAGCTTGG	1215

QY	1132	CATTATGAAGACTACACAAAGGGTAAACGGTAT	1191
DB	1216	CATTATGAAGACTTTCACAAAGGGTAAACGGT	1275
QY	1192	AATGATCTACGTAATATTTGATTTTTCAGAAAT	1251
DB	1276	AATAATCCAGTAAATATTTTGGCNAATACCGAT	1335
QY	1252	A---TCATGAACCTAGTAGGAGAGACTACCGCT	1308
DB	1336	AGATATGCAATGCAACCGTTTGTGGGTATTTCA	1395
QY	1309	GATTTTTCGTAGGTTAGGGGACCTGATTTAAAT	1368
DB	1396	GAAATTTTTTCCGACAAACACTAAATACTTTCT	1452
QY	1369	AGGATGACAAATTTGAATCTACGTTTCCACTTGT	1422
DB	1453	TCACAGACAATTTGAATCTGTGTACCAGGTATT	1512
QY	1423	GGACCTCTCATAGATTAATCAAAATCGGCATGT	1482
DB	1513	AATTAATCTCTCATAGATTAATCAAAATCGGCAT	1572
QY	1483	GTATATGGTTGGACACATACAAGTTTAAACGTC	1542
DB	1573	GTATTTGGTTGGACACATACAAGTATGAAAAGAG	1632
QY	1543	ACACAAATAACCGCGGTGAAGAGTTATTAATTA	1602
DB	1633	ACGCAAAATTCCTGCAAGTAAAGCTTTTGGCCCT	1692
QY	1603	TATGTAATAAAAGGCACCT 1620	
DB	1693	TACGTACACAGCTGGGCGCT 1710	

RESULT 6					
ID	ADR89416	standard; cdna; 2010 BP.			
XX	ADR89416;				
XX	18-NOV-2004 (first entry)				
XX	AXMI-008 alternative start site coding sequence.				
ss	gene; delta-endotoxin; delta-endotoxin associate polypeptide;				
expression cassette; transgenic; plant; bacteria;					
lepidoptera; coleoptera; pest; pesticide; resistance;					
pesticidal activity.					
OS	Bacillus thuringiensis.				
Key	Location/Qualifiers				
1..2010					
/*tag= a					
/product= "Alternative AXMI-008"					
WO2004074462-A2.					
02-SEP-2004.					
20-FEB-2004; 2004WO-US005829.					
20-FEB-2003; 2003US-0448632P.					
20-FEB-2003; 2003US-0448633P.					
20-FEB-2003; 2003US-0448797P.					
20-FEB-2003; 2003US-0448806P.					
20-FEB-2003; 2003US-0448810P.					
20-FEB-2003; 2003US-0448812P.					
19-FEB-2004; 2004US-00781979.					
19-FEB-2004; 2004US-00782020.					

PR 19-FEB-2004; 2004US-00782096.
 PR 19-FEB-2004; 2004US-00782141.
 PR 19-FEB-2004; 2004US-00782570.
 PR 19-FEB-2004; 2004US-00783417.
 XX
 PA (ATHE-) ATHENIX CORP.
 XX
 PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
 XX
 DR WPI; 2004-635574/61.
 DR P-PSDB; ADR89417.
 XX
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
 PT for producing organisms with pesticide resistance.
 XX
 PS Claim 1; SEQ ID NO 28; 178pp; English.
 XX
 CC This sequence encodes an isolated delta-endotoxin. Some of the delta-
 CC endotoxin coding sequences of the invention have alternative start
 CC codons, producing more than one protein from a single open reading frame.
 CC The nucleic acid sequences of the invention are useful in DNA constructs
 CC or expression cassettes for transformation and expression in plants and
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for
 CC killing lepidopteran or coleopteran pests. Compositions containing the
 CC delta-endotoxins of the invention, and methods for their production, are
 CC useful for the production of organisms with pesticide resistance,
 CC specifically bacteria and plants. These organisms are useful for
 CC generating altered or improved delta-endotoxin or delta-endotoxin-
 CC associated proteins that have pesticidal activity, or for detecting the
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
 CC nucleic acids in products or organisms.
 XX
 SQ Sequence 2010 BP; 557 A; 324 C; 417 G; 612 T; 0 U; 0 Other;
 Query Match 35.5%; Score 739.8; DB 13; Length 2010;
 Best Local Similarity 69.7%; Pred. No. 4.8e-158;
 Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;
 10 ATGAGTCCATATCAAAATAAATAATGAATATGAATATTTGGAAATCCTCATCGAATAACACA 69
 1 ATGAAATCTTTATCAAAATACAAATGAATATGAATATTTGGAAATCCTCATCGAATAACACA 60
 70 AATACGCCAACAGATATCTTTTGGCAATATCGGGATATGCTACTATGCTTCTTGAAT 129
 61 AATATGTCAACAGATATCTTTTGGCAATATCGGGATATGCTACTATGCTTCTTGAAT 120
 130 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAAGTAT 189
 121 GCTTGTGAGGGAAGCCATGGCAAGATACCTGGGAATCAGTCGGATATAGTAATAT 180
 190 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAATACATATTA 249
 181 GGGACATACCTTATACAAATCTTGTGTAAGACCCGGTATAGGTGGAATCTCTGTAATAT 240
 250 TCAATATAGGAACCTAATTCGCACTAATCGTCAAACTGTGTGCAGACCTTCTATATGT 309
 241 TCAATATAGGAACCTAATTCGCACTAATCGTCAAACTGTGTGCAGACCTTCTATATGT 300
 310 GATTATATATCTAATATCTGTAAGAGGTAGCCGATAGTGTGTTTAAGTGTATGCGATTGCA 369
 301 GATTATATATCTAATATCTGTAAGAGGTAGCCGATAGTGTGTTTAAGTGTATGCGATTGCA 360
 370 GATTATGAGGTAAATTTGAAAAATTATAGAGAGTATATCTTTCTTATCTTGGGCTTGG 429
 361 GATTATGAGGTAAATTTGAAAAATTATAGAGAGTATATCTTTCTTATCTTGGGCTTGG 420
 430 CTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGCAATTAGTTTAT 489
 421 CTTACAG-----ATAAATCAATTCCTTAAATAAATCTGTCGACGTAGTTTAA 465
 490 TATTTTAAATCTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCATTGTCAGAAAC 549

Db 466 CAGTTCCAGACACGGGAAGAAGATTTCACTAAACTTTTAGCAGGGTCATTATCAAGACAG 525
 QY 550 AATGCTCAGTATTTGTTATTTACCTACTTTTGCACAGCTGCAAAATGTCGAGTATTTACTA 609
 Db 526 AAAGCTGAAATATTTATTTGCTACGTATGTGCAAGCTGCAAAATGTCGATTTATTTACTA 585
 QY 610 TTAAGGGATGCAAGTTCAATATATAAAGCACAAATGTTTCCCAATTTTGTAGTCAGAGAATGTA 669
 Db 586 TTAAGGGACGCAATTAATATATAAAGAAAGATGCGGACTAGTGTGCCACCGTTGTATCCA 645
 QY 670 AGATCGGAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTAATCTATAGCGA 729
 Db 646 GGGTCAGGAGAA-----CTGATTTGTAACGAGCG 675
 QY 730 TTAATAATGCAAAACGGCAGAGTATACCAATTTATTTATATATGTTATGTTATGTTAGT 789
 Db 676 TTAATAATGCAAAATTAATAAGAGTATTAATTTATTTGTTAGGTGGTATTAACAGGGTTTA 735
 QY 790 AATCAGATATAAACACGGGGGACAGTGTCTGACACTTGGTGCATAATTTAATAAATTTCTGT 849
 Db 736 GATCAGATAGACACGGCGGTACAGTGTGCTGAAGTTTGGTGCATAATTTAATAAATTTCTGT 795
 QY 850 AGAGAAATGACGTTGGCGTATTTGGATATTTATCGCTATATTTTCCAACTTATGATTTGAG 909
 Db 796 AGAGAAATGACGTTGGCGTATTTGGATATTTATCGCTATATTTTCCAACTTATGATTTGAA 855
 QY 910 AATATCCATTTCCCAACACATGTAGATGCTAGGGAATTTATACAGATGCAAGTGGGA 969
 Db 856 AATATCCATTTAGCAACAGTGTAGATTTAACTAGGGAATTTATACAGATGCAAGTGGGA 915
 QY 970 TATTCATCGGGAACCTATATAGTTGGTTTACGGAATTTGGCCTTAATCTTTTAAATGGTGTAG 1029
 Db 916 TATTCAGGGGGAATTTATGTTGGGAACGGTTTT-----TTAGCTTTAATTTCCGTAGAA 969
 QY 1030 GCTAATGGAACACGGGGACCTGTTAGTTACTTGGCTTTAGCAAAATAGGTATATATAAT 1089
 Db 970 GCAATGGAACACGGGGACCTGTTAGTTACTTGGCTTTAGCAAGCTATAGATATATATAGT 1029
 QY 1090 GAGTATGTT-----TCGAGATATTTTGGCGCTGGGTAGGAACCTGCTATATGAA 1140
 Db 1030 CATTCATTTAATCTTTCAGCTTGTATCTTAGTGGCTGGGGGGAACCTGCTATATGAA 1089
 QY 1141 GACTACACAAAGGGTAACGGTATTTTCAACGTATGCTCGGAACCTACGAGTAAATGATCTA 1200
 Db 1090 GACTTCACAAAGGGTAACGGTCTTTTCAACGTATGCTCGGAACCTACGAGTAAATGATCTA 1149
 QY 1201 CGTAATATTTGATTTTTCAGAAATGCCGATGTATATAAATTTACTTCAATTAGCTA---TCATG 1257
 Db 1150 CGTAATATTTTTCGGCAATACCGATATATTTTAAATTTTATTTTCAATTAGCTATGCA 1209
 QY 1258 AACCTAGTAGGAGACCTACCGCTAGACACGAGTATCGTGTTCGTTTCAAGGCGCAGATTTTCGT 1317
 Db 1210 ATGCAACCGTTTGTGGGTATTTCAATCCACCGCATCTTGTTCACGTGCGAGAAATTTT 1269
 QY 1318 AGGTTAGGGGACCTGATTTTAAATTTATGATGAGGTAAATAATGGGCTAGCAGGATGACA 1377
 Db 1270 CCGCAACACACTAATATCTTCTGTAGGTAACAGTCTCGGG---TACTCACAGACA 1326
 QY 1378 ATTGAATCTACGTTCCCACTTGT-----ATTGCACCTCTAAATGGTGTGTAGAGGACCTCT 1431
 Db 1327 ATTGAATCTGTGTACCAAGTATTAATAGGATCTTACCACCTAGTCGTACAAATTTACTCT 1386
 QY 1432 CATAGATTAATCAAAATCGGCGATGTTGTATATGGAACCTCCAGAGTTAAACGTATATGTT 1491
 Db 1387 CATAGATTAATCAAAATCGGCGATGTTGTCAAAATGAAACCTCCAGAGTTAAACGTATTTGT 1446
 QY 1492 TCGACACATACAAAGTTTAAACCTGCAATATAAATTTGAGCCCAATCAAAATTTACACAAATA 1551
 Db 1447 TCGACACATACAAAGTATGAAATAAATATCGAATTTATTCAGATAAATAATTCAGCAATTT 1506
 QY 1552 CCGGCGGTGAGAGGTTTATTTACCTTCAAAATTTATCTTGTAAATGCTCTATATCTATGTAATA 1611
 Db 1507 CTTGCAAGTAAAGCTTTTGGCCCTCACGACGAGTACAGGATATGCAAGGAGTTACGTCACA 1566


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QY      1612 AAAGGCACT 1620
Db      1567 GCTGGGCGCT 1575

RESULT 7
AAZ93234
ID      AAZ93234 standard; DNA; 1983 BP.
AC
XX
XX      AAZ93234;
DT      04-JUL-2000 (first entry)
DE      Sequence encoding truncated Cry9Aa toxin.
XX      Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
KW      ds.
XX
XX      Synthetic.
OS      Bacillus thuringiensis; ssp. galleria.
XX
XX      Key      Location/Qualifiers
FH      17..1966
FT      /*tag= a
FT      /product= "Cry9Aa toxin N-terminal fragment"
XX
XX      WO200011025-A1.
XX
XX      02-MAR-2000.
XX
XX      24-AUG-1999; 99WO-FI000698.
XX
XX      24-AUG-1998; 98FI-00001809.
XX
XX      (UNIC-) UNICROP LTD.
XX
XX      Kuvshinov V, Kanerva A, Koivu K, Pehu E;
XX
XX      WPI; 2000-224660/19.
DR      P-PSDB; AAY83039.
XX
XX      Modified synthetic DNA sequences comprise modification of the truncated
XX      cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX      plants.
XX
XX      Claim 2; Page 55-57; 90pp; English.
XX
XX      Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
XX      gene of Bacillus thuringiensis ssp. galleria can be used for the
XX      production of a unique insecticidal protein having the same properties as
XX      the N-terminal domain of the insecticidal protein encoded by the native
XX      cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
XX      toxin works by binding to specific receptor molecules in the gut of
XX      insects with consequent formation of ion channels in the epithelium. This
XX      action leads to ion efflux and paralysis of the intestinal function.
XX      which causes death of the insect. The synthetic DNA sequences exhibit
XX      enhanced expression through improved mRNA processing, stability, and/or
XX      translation providing improved tolerance against target insects. They can
XX      be used in the production of transgenic plants capable of expressing the
XX      N-terminal domain of the insecticidal protein encoded by the native
XX      cry9Aa gene. They therefore have a role in pest control and crop
XX      protection
XX
XX      Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;
XX
XX      Query Match      8.2%; Score 170.2; DB 3; Length 1983;
XX      Best Local Similarity 52.6%; Pred. No. 1.3e-28;
XX      Matches 459; Conservative 0; Mismatches 363; Indels 51; Gaps 2;
XX
QY      156 AATTGGGAATCAGTCGAAACGACATACAAAGTATTTGGGATAAAATCTTTATAGATTTGTGAT 215
Db      139 AATAGCGATGCGAGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 198

216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
199 AGCACCTTCTCTTACTGGAATTAATTTCAATAGTATATGACCTTATAGGTAAAGTAGTAGG 258
270 TCCGACTAATCGTCAAACTGTGTGACGACATTTCTATATGCTGATTTATTTATCTATAATTCG 329
259 AGGTAGTAGTGAGCAATCCATATCAGATTTGTCTATATGTGACTTTATTTATCTATTATGA 318
330 TAAAGAGGTAGCCGATAGTGTGTTTAAAGTGATGCGAATTCAGATTTTGAACGGTAATTTGAA 389
319 TTTACGGGTAACTCAGAGTGTGTTTAAATGATGGGATTCAGATTTTAAATGTTCTGTACT 378
390 AAATATATAGAGATTTATATCTTTCTTATCTTTGGGGCTTGGCTTAAAGACGGTAACCACT 449
379 CTTATACAGGAATATTTAGAGGCTCTGGATAGCTGGAATAAGAAATCCTAATTTCTGCTTC 438
450 TCARAAGACAATAATTTCTGATATCGGCAATTAGTTTATTTATTTTAAACTTTTCAGAAG 509
439 TGCTGAAGAACTCCGTACTCGTTTGTAGAAATCGCGACTCAGAAATTTGTAGAAATTTTAAAC 498
510 AGATTTCAATGAAATTTCTAGGAGGCTCATTTGTCAAGAAACAATGCTCAAGTATTGTTATT 569
499 CCGAGGCTCTTTAAGCAATGCTGCTCGTTAGCTAGACAAATGCCCAATATTATTATT 558
570 ACCTACTTTTGCACAAGCTGCAAAATGTGCAATTTACTATTAAAGGGATGAGTTCAATA 629
559 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTTACTTACTTAAGGGATGCTACTAGATA 618
630 TAAAGCACAAATGGTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689
619 TGGCACTAATTTGGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAAACTAGT 678
690 TAACAGATGCTGTGATTTTACCGGTGATTTACTATGAGCGATTAAAAATCAAAACCGGCAGA 749
679 AGAGCTTATT-----GNACT 693
750 GTATACCAATTTATTTTATATTTGATATGCTATGCTAGGTGTTTAAATCAGATAAAACAGGGGG 809
694 ATATACTGATTTATTCGCTACATTTGCTATAATCGAGGTTTCAACGAACTAAGACAGAGG 753
810 GACAGGCTCTGACACTTGGTCGAAATTTAAATAATTTCTAGAGAAATGACGTTGGCGGT 869
754 CACTAGTCTACAGCTTGGTTAGAAATTTCTAGATATCGTAGAGATGACATTTGATGCT 813
870 ATTGATATTATCGCTATATTTTCCAACCTTATGATTTTGAGAAATATCCATTGCCAACACA 929
814 ATTAGATATAGTACATCATTTTCAAGTCTTGATATTACTAATTACCCCAATAGAAACAGA 873
930 TGTAGATTTGACTAGGAAATTTATACAGATGCTAGTGGGATATTTCATCGGAACTTATAG 989
874 TTTTCAGTTGATAGTGGGTCAATTTATACAGATCCAAATGTTGTTTGTACATCGTAGTGTCT 933
990 TTGGTTACGGAATTTGGCTTAATCTATTTTAAATGG 1022
934 TAGGGGAAAAGTTGGTTTACCTTTGTTAATAG 966

RESULT 8
AAZ93235
ID      AAZ93235 standard; DNA; 3837 BP.
XX
XX      AAZ93235;
AC
XX
XX      15-SEP-2003 (revised)
DT      04-JUL-2000 (first entry)
XX
XX      Sequence encoding native Cry9Aa toxin.
DE
XX      Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
KW      ds.
XX
XX      Bacillus thuringiensis; ssp. galleria.
OS

```


XX Key Location/Qualifiers
 PH 385..2364
 FT /*tag= a
 FT /product= "Cry9Aa toxin"
 PN W0200011025-A1.
 XX
 XX 02-MAR-2000.
 XX
 XX 24-AUG-1999; 99WO-F1000698.
 XX
 XX 24-AUG-1998; 98FI-00001809.
 XX
 XX (UNIC-) UNICROP LTD.
 XX
 XX Kuvshinov V, Kanerva A, Koivu K, Pehu B;
 XX
 XX WPI; 2000-224660/19.
 DR P-PSDB; AAY82988.
 XX
 XX Modified synthetic DNA sequences comprise modification of the truncated
 PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in
 PT plants.
 XX
 XX Claim 10; Page 57-59; 90pp; English.
 XX
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
 CC gene of *Bacillus thuringiensis* ssp. *Galleria* can be used for the
 CC production of a unique insecticidal protein having the same properties as
 CC the N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene of *Bacillus thuringiensis* ssp. *Galleria*. The insecticidal
 CC toxin works by binding to specific receptor molecules in the gut of
 CC insects, with consequent formation of ion channels in the epithelium. This
 CC action leads to ion efflux and paralysis of the intestinal function,
 CC which causes death of the insect. The synthetic DNA sequences exhibit
 CC enhanced expression through improved mRNA processing, stability, and/or
 CC translation providing improved tolerance against target insects. They can
 CC be used in the production of transgenic plants capable of expressing the
 CC N-terminal domain of the insecticidal protein encoded by the native
 CC cry9Aa gene. They therefore have a role in pest control and crop
 CC protection. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 XX Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;
 SQ

Query Match 8.2%; Score 170.2; DB 3; Length 3837;
 Best Local Similarity 52.8%; Pred. No. 1.6e-28;
 Matches 459; Conservative 0; Mismatches 363; Indels 51; Gaps 2;

QY 156 AATTGGGAATCAGTCGAAACGATAACAAGTATTGGGATAAATCTTTATAGAGTTTCTGTAT 215
 DB |||||
 QY 216 AGAACCTAGTTGGGTGGGAATTAAATACATTTAT-----CAATAATAGGAAATTAAT 269
 DB |||||
 QY 597 AGCACCTTCTTCTTACTGGATTAAATTTCAATAGTATATGACCTTTATAGGTAAGTACTAGG 656
 DB |||||
 QY 270 TCGACTAATCGTCAACATGTGTTCAGCAGCTTCTATATGTGATTTATCTATATATTCG 329
 DB |||||
 QY 657 AGGTAGTAGTGGCAATCCATATCAGATTGTCTATATGTGACTTATCTATTTATTTGA 716
 DB |||||
 QY 330 TAAAGAGTAGCCGATAGTGTGTTTAAAGTGTGATGCGATTGTTGACGGTAAATTTGAA 389
 DB |||||
 QY 717 TTTACGGGTAGTCAGAGATGTTTAAATGATGGATGCGAGATTTAATGGTTCTGTACT 776
 DB |||||
 QY 390 AAATTATAGAGATATTATCTTTCTTATCTTTGGGCTTGGCTTAAAGACGGTAAACCACT 449
 DB |||||
 QY 777 CTTATACAGAACTATTATAGAGCTCTGGATAGCTGGAATAAGAACTCTTAATCTGCTTC 836
 DB |||||
 QY 450 TCAAAAGACAATAATCTTGATATCGACAATTAGTTTATTTATTTAACTTTTCAGAAAG 509
 DB |||||
 QY 837 TCGTGAAGAACTCCGCTACTCGTTTGTAGAAATCGCCGACTCAGAAATTTGATAGAAATTTAAC 896
 DB |||||

QY 510 AGATTTCAATGAATTTCTAGGAGGTCATTTGTCAGAAACAAATGCTCAAGTATTTGTTATT 569
 DB |||||
 QY 897 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGTCAGCAAAATGCCCAATATTTATTATT 956
 DB |||||
 QY 570 ACTACTTTTGCACAAAGTCGCAAAATGTGCAAGTTATTACTATTAAAGGATGCAAGTCAATA 629
 DB |||||
 QY 957 ACCTTCTTTTGGAGCGCTGCATTTTTCATTTATTACTTAAGGGATGCTACTAGATA 1016
 DB |||||
 QY 630 TAAAGCACAATGGTTCCTCCATTTTGTAGTCAGAGAAATGTAAGATCGGAATTAATATCACC 689
 DB |||||
 QY 1017 TGGCATAATTTGGGGCTATACAATGCTACACCTTTATAAATTTATCAATCAAAATAGT 1076
 DB |||||
 QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTAAAAATGCAAAACGCGAGA 749
 DB |||||
 QY 1077 AGAGCTTATT-----GAACT 1091
 DB |||||
 QY 750 GTATACCAATATTGTTTATATTGTTATTCAGGTAGTGTTTAAATTCAGATAAACAGGGGG 809
 DB |||||
 QY 1092 ATATACCTGATTATTGGTATACATTTGGTATAATCGAGGTTTCAACGAACTAAGACAAGGAG 1151
 DB |||||
 QY 810 GACAGTGTGACACCTTGGTCGAAATTTAAATTAATTTTCGTAGAGAAATGACGTTGCGGCT 869
 DB |||||
 QY 1152 CACTAGTGTACAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGAGATGACATTTGATG 1211
 DB |||||
 QY 870 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTTGCCAACACA 929
 DB |||||
 QY 1212 ATTAGATATAGTAGATCATTTTCAAGTCTTGATATTACTATTACCCAAATAGAAACAGA 1271
 DB |||||
 QY 930 TGTAGAGTTGACTAGGGAATTTTATACAGATCAGTGGGATATTCATCGGGAACCTTATAG 989
 DB |||||
 QY 1272 TTTTCAGTTGAGTAGGCTCATTTATACAGATCCAAATTTGTTTGTATACATCGTAGTAGTCT 1331
 DB |||||
 QY 990 TTGGTTACGGAATTTGCCCTAACTTTTAACTG 1022
 DB |||||
 QY 1332 TAGGGGAGAAAGTTGGTTTGGCTTTGTTTAATAG 1364
 DB |||||

RESULT 9
 AAV16515
 ID AAV16515 standard; DNA; 3471 BP.
 AC AAV16515;
 XX
 XX 11-JUN-1998 (first entry)
 XX
 XX DNA encoding a *Bacillus thuringiensis* toxin designated 86BB1(a).
 DE Toxin; lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;
 KW *Heliothis virescens*; *Helicoverpa zea*; ss.
 KW
 XX *Bacillus thuringiensis*.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3471
 FT /*tag= a
 XX
 XX W09800546-A2.
 XX
 XX 08-JAN-1998.
 PD
 XX 01-JUL-1997; 97WO-US011658.
 PF
 XX 01-JUL-1996; 96US-00674002.
 PR
 XX (MYCO) MYCOGEN CORP.
 PA
 XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;
 PI
 XX WPI; 1998-086971/08.
 DR
 XX P-PSDB; AAW46856.
 PT New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes
 encoding toxins which are active against lepidopteran pests such as the

Db 393 CTTATACAGAACTATTAGAGGCTCTGGATAGCTGGAATAAGAAATCCTTAATCTCGTTC 452
Qy 450 TCAAAAGACAAATAATCTGATATCGACAAATAGTTTATTATTATTTAAACTTTCAGAAAG 509
Db 453 TGCTGAGAACTCCGTACTCGTTTATAGAAATCGCCGACTCAGAAATTTGATAGAAATTTAAAC 512
Qy 510 AGATTTCATGAAATTTCTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569
Db 513 CCGAGGCTCTTTAAAGAAATGGTGGCTGTTAGCTAGACAAATGCCCAATATATTATT 572
Qy 570 ACTTACTTTTGCACAAAGTGCAGTATTTACTATTATTAAGGGATGCGAGTTCAATA 629
Db 573 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTATTACTACTAAGGATGCTACTAGATA 632
Qy 630 TAAAGCACAATGCTTCCCATTTTGTAGTCAGAGAAATGAAGATCGGAATTAATATCACC 689
Db 633 TGGCACTAATTTGGGGCTATACAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
Qy 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACCAATATTGTTTATATTGGTATCAGTAGGTTTAAATPCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTATTGCGTACATTGGTATATATCGAGGTTTCAACGAACTAAGCAACGAGS 767
Qy 810 GACAGTGTCTGACACTTGTGCGAAATTAATAATTCGTAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTCTACAGCTTGGTGAATTTTCATGATATCGTAGAGATGACATTTGATGT 827
Qy 870 ATTGATATTATCGCTATATTCCCACTTATGATTTTGAGAAATATCCATGCGCACACA 929
Db 828 ATTAGATATTAGTAGCATTTTCAAGTCTTGATATTACTAATTTACCAATAGAAACAGA 887
Qy 930 TGTAGATTGACTAGGGAATTTTATACAGATGAGTGGGATTTTCATCGGGAATTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAAATGGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGAATGGCCTAACTACTTTTAATGG 1022
Db 948 TAGGGAGAAAGTTGGTTAGCTTTTGTAAATAG 980

RESULT 11

AAS02478
ID AAS02478 standard; DNA; 2407 BP.

AC AAS02478;

XX 29-AUG-2001 (first entry)

DE B. thuringiensis DNA encoding a toxic crystal protein, CryET60.

XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;
KW cotton leaf perforator; CryET60; ds.

OS Bacillus thuringiensis.

XX Key Location/Qualifiers
FH 1..2406
CDS /tag= a
FT /product= "CryET60"
FT /partial
FT /note= "No stop codon"

XX WO200119859-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US025361.
PF
XX 15-SEP-1999; 99US-0153995P.
XX (MONS) MONSANTO CO.
XX
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;
XX WPI; 2001-281518/29.
DR P-PSDB; AAU02035.
XX
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides
XX and the polynucleotides that encode them, useful for increasing the
XX insect resistance of plant.
XX
XX Claim 17; Page 127-128; 173pp; English.
XX
XX The sequence encodes a B. thuringiensis Lepidopteran-active delta-
XX endotoxin, crystal protein CryET60. The Lepidopteran-active B.
XX thuringiensis delta-endotoxin polypeptides may be used as compositions
XX that are applied to plant crops to protect them from insect damage. The
XX polynucleotides may be used in the production of transgenic plants that
XX express the insecticidal polypeptides and consequently have improved
XX insect resistance compared to non-transformed plants. Monocotyledonous or
XX dicotyledonous plants may be protected in this way, for example corn,
XX wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,
XX tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,
XX fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree
XX cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,
XX cotton leaf perforator and spruce budworm) may be affected by application
XX of the insecticidal polypeptides (full details given in specification)
XX
SQ Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;

Query Match 7.7%; Score 160.6; DB 4; Length 2407;
Best Local Similarity 51.9%; Pred. No. 2.1e-26;
Matches 453; Conservative 0; Mismatches 369; Indels 51; Gaps 2;
Qy 156 AATTTGGGAATCAGTCGAAACGATTAACAGTATTTGGGATAAATCTTTATAGATTTCTGAT 215
Db 153 AATAGCGATGCGCAAAAGAGAGTATCTATTGGGACACCATAGTCTCTCTTATCAC 212
Qy 216 AGAACCTAGTTTGGGTGGATTAATACACTATTAT-----CAATAATAGGAACATAAT 269
Db 213 AGCACCTTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG 272
Qy 270 TCCGACTAATCGTCAAACTGTCTCAGCACTTTCTATATGTGATTATTATCTATAATTCG 329
Db 273 AGGTAGTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATTTATTTATTTGA 332
Qy 330 TAAAGAGGTAGCCGATAGTGTTTTAAAGTATCGGATTCGAGATTTTGACGGTAAATTTGAA 389
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGATTCGAGATTTTAAATGGTCTCTACT 392
Qy 390 AAATTATAGAGATTTATCTTTCTTATCTTGGGCTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAATCTTTTAGAGGCTCTGGATAGCTGGAATAAGAATCCFAATTTCTGCTTC 452
Qy 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATAGTTTATTATTATTAAAACTTTTCAGAAAG 509
Db 453 TGCTGAAGAACTCCGTACTCGTTTAGAATCCCGCACTCAGAAATTTGATAGAAATTTAAC 512
Qy 510 AGATTTCATGAATTTCTAGGAGGGTCATTTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569
Db 513 CCGAGGCTCTTTAAAGAAATGGTGGCTCGTTAGCTAGACAAATGCCCAATATATTATT 572
Qy 570 ACTTACTTTTGCACAAAGTGCAGTATTTACTATTAAAGGATGCGAGTTCAATA 629
Db 573 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTATTACTACTAAGGATGCTACTAGATA 632
Qy 630 TAAAGCACAATGTTTCCCATTTTGTAGTCAGAGAAATGTAAGATCGGAATTAATATCACC 689

Db 633 TGGCACTAATTGGGGCTATACAATGCTACACCTTTTATAATTATCAATCAAACTAGT 592
 QY 690 TAAACAGTGGTGTGATTTTACCAGGTGATTAATGAGCGATTAATAATGCAAAACGGCAGA 749
 Db 693 AGAGCTTATT-----GAACT 707
 QY 750 GTATACCAATTTTGTATATTTGGTATCAGGTAGGTTTAAATCAGATAAACACGGGGG 809
 Db 708 ATATAGTATGATTTTGGTATGATTTGGGATTAATCAGGTTTCAACCGAACTAAGACAACGAGG 767
 QY 810 GACAGTGTCTGACACTTGGTGCAGAAATTTAATAAATTTCTAGAGAAATGACGTTGGCGGT 869
 Db 768 GCCTAGTGTACAGCTTGGTGTAGATTTTCATAGATATCGAGAGAGATGACATTTGATGG 827
 QY 870 ATGATATATTCGCTATATTTCCAACTTATGATTTTGGAGAAATATCCATTCGCAACACA 929
 Db 828 ATTAGAAATAGTAGCATCATTTTCAAGTCTGATATTACTAATTAACCAATAGAAACAGA 887
 QY 930 TGTAGATTGACTAGGGAATTTATACAGATGCGATGGGATATTCATCGGGAATTTATAG 989
 Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCAATTTGGTTTGTACATCGTAGTAGTCT 947
 QY 990 TTGGTTACGGAATTGGCCTAATACTTTTAAATGG 1022
 Db 948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

RESULT 12

ABX13497
 ID ABX13497 standard; DNA; 4366 BP.
 XX AC ABX13497;
 XX DT 27-OCT-2003 (revised)
 DT 29-MAY-2003 (first entry)
 XX DE B. popilliae parasporal body-associated polynucleotide SEQ ID 19.
 XX KW Parasporal body; insect; larva; growth inhibiting; insecticidal;
 KW Scarabaeidae; turf; agricultural crop; tree; proteinaceous aggregate;
 KW Anomala cuprea; horticultural crop; gene; ds.
 XX OS Paenibacillus popilliae; subsp semadara.

Key Location/Qualifiers
 CDS 224..4258
 FT /*tag= a
 FT /product= "parasporal body-associated protein"
 XX US2002182693-A1.
 XX 05-DEC-2002.
 XX 12-APR-2002; 2002US-00120544.
 XX 13-APR-2001; 2001JP-00115754.
 PR 04-JUL-2001; 2001JP-00203463.
 XX (DNIN) DAINIPPON INK & CHEM INC.
 XX Tanaka M, Yokoyama T, Aoyagi M, Hasegawa M, Ehara G, Kimura M;
 PI Nishinashi H;
 XX WPI; 2003-328619/31.
 DR P-PSDB; ABG74771.

XX New polypeptide having a larvae growth inhibiting or insecticidal effect
 PT in a Scarabaeidae insect, useful for controlling Scarabaeidae insect in
 PT turf, agricultural crops or trees.
 XX Claim 12; Page 37-42; 54pp; English.
 XX This invention describes a novel parasporal body-associated polypeptide

CC which has larval growth inhibiting or insecticidal effect in members of
 CC the Scarabaeidae insect family. The polypeptides and agents derived from
 CC the polypeptides of the invention are useful for controlling Scarabaeidae
 CC insects. Larvae of the Scarabaeidae insects eat the roots of a wide
 CC variety of plants e.g turf, agricultural or horticultural crops and
 CC trees, causing serious damage. This sequence encodes a polypeptide
 CC associated with the parasporal body contained in the sporangia of
 CC bacterium belonging to the Bacillus family. The parasporal body is a
 CC proteinaceous aggregate which comprises one kind or different kinds of
 CC polypeptides. The products of the invention have been shown to have a
 CC controlling effect on Anomala cuprea. (Updated on 27-OCT-2003 to
 CC standardise OS field)

SQ Sequence 4366 BP; 1383 A; 836 C; 976 G; 1171 T; 0 U; 0 Other;

Query Match 4.9%; Score 102.4; DB 8; Length 4366;
 Best Local Similarity 58.0%; Pred. No. 4.1e-13;
 Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;
 QY 716 ATTACTATGAGCGGATTAAATGCAAAACGGCAGAGTATACCAATTTATTTTATATTGTT 775
 Db 921 ATAATTACAATCGCCCAACAAAGGAACCTCCGCAACGTATGCAAAATCAITTTGTAACACTTGT 980
 QY 776 ATCAGGTAGGTTTAAATCAGATAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 835
 Db 981 ATCAGACGGTTTACA-----AGATTGCAAGGCGAGCTAGCAGTTGGGTCNAAT 1034
 QY 836 TTAATAAATTTCTAGAGAAATGACGTTGGCGGTATTCGATATATATCGCTATATTTCCAA 895
 Db 1035 ATAATCGATTTAGAGAGAAATAACGTTAATAGTATTTGGATATTTGTGCTATTTTCAA 1094
 QY 896 CTTATGATTTTGAGAAATATCCATTCGCAACACATGTAGAGTTGACTAGGGAATTTATA 955
 Db 1095 ATTATGATGTTTGTAGTTATCCAAATACAGTTACGGGGAGAGCTTACGAGAGGAATTTATA 1154
 QY 956 CAGATGCGAGTGGGATATTATTCGGAACCTTATAGTTGGTTACGGAATTTGGCCTAATCTT 1015
 Db 1155 CGATCCAGCAGTATATAGCGGTACAGGTTCTTATCTCTGTTGAGTCAAGCACCATCAT 1214
 QY 1016 TTAATGGTTTAGAGCTAATGGAACACCGGGACCTGGTTTGTAGTTACTTTGG 1065
 Db 1215 TTGCAGAAATAGAAAATATCGCAATTAGGGAACCAAGCAATTTTACTTTGG 1264

RESULT 13
 AEB90830
 ID AEB90830 standard; DNA; 4366 BP.
 XX AC AEB90830;
 XX DT 06-OCT-2005 (first entry)
 XX DE Paenibacillus popilliae parasporal body gene SeqID19.
 XX KW insecticide; crop improvement; plant insect pest; pesticide;
 KW protein purification; gene; ds.
 XX OS Paenibacillus popilliae.

Key Location/Qualifiers
 CDS 224..4258
 FT /*tag= a
 FT /product= "Bacillus popilliae parasporal body protein
 SeqID20"
 XX US2005172355-A1.
 XX 04-AUG-2005.
 XX 29-MAR-2005; 2005US-00091654.
 XX 13-APR-2001; 2001JP-00115754.
 PR 04-JUL-2001; 2001JP-00203463.

PR 12-APR-2002; 2002US-00120544.
XX (DNIN) DAINIPPON INK & CHEM INC.
XX Tanaka M, Yokoyama T, Aoyagi M, Hasegawa M, Ehara G, Kimura M;
XX Nishinashi H;
XX WPI; 2005-563092/57.
DR P-PSDB; AEB90831.
XX
XX New isolated polynucleotide encoding a protein having a larvae growth
PT inhibiting or insecticidal effect on Scarabaeidae insects, useful as a
PT controlling agent or insecticide against Scarabaeidae insects such as
PT Anomala cuprea.
XX
XX Claim 28; SEQ ID NO 19; 53pp; English.
XX
XX This invention relates to a novel isolated polynucleotide and the encoded
CC protein which has a larvae growth inhibiting or insecticidal effect on a
CC Scarabaeidae insect. The invention may be useful for the development of
CC compounds with an insecticide activity. The polypeptide encoded by the
CC polynucleotide is useful as a larval growth inhibitor or insecticide
CC against Scarabaeidae insects such as Anomala cuprea. The polypeptide can
CC be applied to turf (for example golf courses), agricultural crops (for
CC example sweet potato or peanuts), or trees. Larvae of Scarabaeidae
CC insects such as Anomala cuprea, Blitopertha orientalis and Popillia
CC japonica have conventionally been controlled by chemical pesticides, but
CC as the larvae are buried in the ground large amounts of pesticide have to
CC be used and there is a need for safer control methods. A polypeptide from
CC Paenibacillus popilliae susp. melolonthae Hi has a controlling effect on
CC Melolontha melolontha (M097/14798) but it was not made clear whether the
CC bacterial strain and polypeptide have controlling effects on Anomala
CC cuprea, Blitopertha orientalis and Popillia japonica. The invention
CC provides new polypeptides obtained by screening Paenibacillus popilliae
CC expression libraries using antisera obtained by immunizing animals with
CC extracts of Paenibacillus popilliae species from infected Scarabaeidae
CC larvae. The new polypeptides are unrelated to the previously identified
CC polypeptide. Tests using the Escherichia coli clones identified in the
CC library screening against Anomala cuprea larvae showed an inhibitory
CC effect on the larvae. The present sequence is that of a gene of the
CC present invention specific to the parasporal body region of Paenibacillus
CC popilliae.
XX
XX Sequence 4366 BP; 1383 A; 836 C; 976 G; 1171 T; 0 U; 0 Other;
SQ

Query Match 4.9%; Score 102.4; DB 14; Length 4366;
Best Local Similarity 58.0%; Pred. No. 4.1e-13;
Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

QY 716 ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTCGTTATATGCT 775
DB 921 ATATTTACAAATGCCAACAAAGAACTCCGCAACGTATGCAATCATNTTACAACTTGT 980
QY 776 ATCAGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGCACCTTGGTCGAAT 835
DB 981 ATCAGACGGGTTTACA-----AAGATTCAAGGCAGCGATGTAGCAGTTCGGTCAAT 1034
QY 836 TTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTTGATATATTCGTTATATTTCCAA 895
DB 1035 ATATATCGATTTAGAGAGAAATAACGTTAATAGTATTTGATATTTGTCATGTTTTCAA 1094
QY 896 CTTATGATTTTGAAGAAATATCATTCGCAACACATGTAGCTTACTAGGAAATTTATA 955
DB 1095 ATTATGATGTTGTTAGTTATCAATACATAGTTACGGGGAGAGCTTACGAGGAAATTTATA 1154
QY 956 CAGATCCAGTGGGATATTCATCGGGAACCTTATATGTTGTTACGGAATTCGCCATACCT 1015
DB 1155 CGGATCCAGCAGTATATACGGGTACAGGTTCTTATTCCTGTTGTTGACGACCATCAT 1214
QY 1016 TTAATGGGTTAGAGGCTTAATGAACACGCGGGACCTGTTAGTTACTTGG 1065
DB 1215 TTGCAGAAATAGAAAATATCGCAATTTAGGGAACCAAGCAATTTTACTTGG 1264

RESULT 14
ADR89411
ID ADR89411 standard; cDNA; 1986 BP.
XX AC ADR89411;
XX 18-NOV-2004 (first entry)
XX AXMI-009 alternative start site coding sequence #2.
DE
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
XX
XX Bacillus thuringiensis.
XX
XX Key Location/Qualifiers
FT 1..1986
CDS /*tag= a
FT /product= "Alternative AXMI-009 #2"
FT
XX WO2004074462-A2.
XX
XX 02-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005829.
XX
XX 20-FEB-2003; 2003US-0448632P.
PR 20-FEB-2003; 2003US-0448633P.
PR 20-FEB-2003; 2003US-0448797P.
PR 20-FEB-2003; 2003US-0448806P.
PR 20-FEB-2003; 2003US-0448810P.
PR 20-FEB-2003; 2003US-0448812P.
PR 19-FEB-2004; 2004US-00781979.
PR 19-FEB-2004; 2004US-00782020.
PR 19-FEB-2004; 2004US-00782096.
PR 19-FEB-2004; 2004US-00782141.
PR 19-FEB-2004; 2004US-00782570.
PR 19-FEB-2004; 2004US-00783417.
XX
XX (ATHE-) ATHENIX CORP.
XX
XX Carozzi N, Hargies T, Kozziel MG, Duck NB, Carr B;
XX WPI; 2004-635574/61.
DR P-PSDB; ADR89412.
XX
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX
XX Claim 1; SEQ ID NO 23; 178pp; English.
XX
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX
XX Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;
SQ

Query Match

4.8%; Score 99.6; DB 13; Length 1986;

Best Local Similarity 59.9%; Pred. No. 1.5e-12;
Matches 187; Conservative 0; Mismatches 119; Indels 6; Gaps 1;
QY 697 GGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAGGAGGAGTATACC 756
DB 619 GGTGATGATGAATTCGTGATTAATATATACAGACTACAAGGACTGATTAGAGATATAA 678
QY 757 AATTATTGTTTATATTTGGTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGT 816
DB 679 GATCATTGTATAAATCTTATAACACAGGCTTTAAATCAATTTAATC-----GCTCAAT 732
QY 817 GCTGACACTTGTGCGAAATTTAATAATTCGTAGAGAAATGACGTTGCGGTATTTGGAT 876
DB 733 GCTCAAGATTGGGTGAGCTTTAATAGGTTTCGTACAGATATGACATTAACAGTATTAGAT 792
QY 877 ATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTCGCAACACATGTAGAG 936
DB 793 CTCGCAATATTTTCCAACTATGATCCAGTAGGTATCCATTTAGCAGTAAACCGGAA 852
QY 937 TTGACTAGGAAATTTATACAGATGCGAGTGGGATATTCATCGGGAACTTTATAGTTGGTTA 996
DB 853 TTGACTAGGAAATTTATACAGATCCAGTAGGTTTACTGCGGTATTACAGAAAGTGGAGT 912
QY 997 CGGAATTGCGCT 1008
DB 913 AGGACTTACCCT 924

RESULT 15
ADR89409
ID ADR89409 standard; cDNA; 2016 BP.
AC ADR89409;
DT 18-NOV-2004 (first entry)
DE AXMI-009 alternative start site coding sequence.
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;
KW expression cassette; transformation; transgenic; plant; bacteria;
KW lepidoptera; coleoptera; pest; pesticide; resistance;
KW pesticidal activity.
OS Bacillus thuringiensis.
FH Key
FT CDS
FT 1. .2016
FT /*tag= a
FT /*product= "Alternative AXMI-009"
XX WO2004074462-A2.
XX 02-SEP-2004.
XX 20-FEB-2004; 2004WO-US005829.
XX 20-FEB-2003; 2003US-0448632P.
XX 20-FEB-2003; 2003US-0448633P.
XX 20-FEB-2003; 2003US-048797P.
XX 20-FEB-2003; 2003US-0448806P.
XX 20-FEB-2003; 2003US-0448810P.
XX 20-FEB-2003; 2003US-0448812P.
XX 19-FEB-2004; 2004US-00781979.
XX 19-FEB-2004; 2004US-00782020.
XX 19-FEB-2004; 2004US-00782096.
XX 19-FEB-2004; 2004US-00782141.
XX 19-FEB-2004; 2004US-00782570.
XX 19-FEB-2004; 2004US-00783417.
XX (ATHE-) ATHENIX CORP.
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

DR WPI; 2004-635574/61.
XX P-PSDB; ADR89410.
PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT for producing organisms with pesticide resistance.
XX Claim 1; SEQ ID NO 21; 178pp; English.
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-
CC endotoxin coding sequences of the invention have alternative start
CC codons, producing more than one protein from a single open reading frame.
CC The nucleic acid sequences of the invention are useful in DNA constructs
CC or expression cassettes for transformation and expression in plants and
CC bacteria. The nucleic acids and corresponding polypeptides are useful for
CC killing lepidopteran or coleopteran pests. Compositions containing the
CC delta-endotoxins of the invention, and methods for their production, are
CC useful for the production of organisms with pesticide resistance,
CC specifically bacteria and plants. These organisms are useful for
CC generating altered or improved delta-endotoxin or delta-endotoxin-
CC associated proteins that have pesticidal activity, or for detecting the
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or
CC nucleic acids in products or organisms.
XX Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;
QY Query Match 4.8%; Score 99.6; DB 13; Length 2016;
DB Best Local Similarity 59.9%; Pred. No. 1.5e-12;
Matches 187; Conservative 0; Mismatches 119; Indels 6; Gaps 1;
QY 697 GGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAGGAGGAGTATACC 756
DB 649 GGTGATGATGAATTCGTGATAATTTATATCAGACTACAAGGACTGATTAGAGATATAA 708
QY 757 AATTATTGTTTATATTTGGTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGACAGT 816
DB 709 GATCATTGTATAAATCTTATAACCCAGGTTTAAATCAATTTAATC-----GCTCAAT 762
QY 817 GCTGACACTTGGTTCGAAATTTTAAATAATTCGTAGAGAAATGACGTTGCGGTATTTGGAT 876
DB 763 GCTCAAGATTGGGTGAGCTTTTAAATAGGTTTCGTACAGATATGACATTAACAGTATTAGAT 822
QY 877 ATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTCGCAACACATGTAGAG 936
DB 823 CTCGCAATATTTTCCAACTATGATCCAGTAGGTATCCATTTAGCAGTAAACCGGAA 882
QY 937 TTGACTAGGAAATTTTATACAGATGCGAGTGGGATTTTCATCGGGAACTTTATAGTTGGTTA 996
DB 883 TTGACTAGGAAATTTTATACAGATCCAGTAGGTTTACTGCGGTATTAGAAAGTGGAGT 942
QY 997 CGGAATTGCGCT 1008
DB 943 AGGACTTACCCT 954

Search completed: December 19, 2005, 14:37:55
Job time : 777.097 secs

Db 181 ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTATTGGGTGGAATTAAT 240
QY 241 ACACATATTCAATAATAGGAAAACTTAATTCGCACTAATCGTCAAACTGTGTGACGACATT 300
Db 241 ACACATATTCAATAATAGGAAAACTTAATTCGCACTAATCGTCAAACTGTGTGACGACATT 300
QY 301 TCTATATGTGATTATTATTATCTATTAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAGTGAT 360
Db 301 TCTATATGTGATTATTATTATCTATTAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAGTGAT 360
QY 361 GCGATTGACAGATTTTGACCGTAAATGAAAAATTATAGAGAGTATTATCTCTTCTTATCTT 420
Db 361 GCGATTGACAGATTTTGACCGTAAATGAAAAATTATAGAGAGTATTATCTCTTCTTATCTT 420
QY 421 GGGGCTTGCTTTAAAGACCGGTAAACCACTTCAAAAAGACAAATAATTCGATATCGGACAA 480
Db 421 GGGGCTTGCTTTAAAGACCGGTAAACCACTTCAAAAAGACAAATAATTCGATATCGGACAA 480
QY 481 TTAGTTTATATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTCCTAGAGGGTCATTG 540
Db 481 TTAGTTTATATTTTAAACCTTTTCAGAAAGAGATTTCAATGAAATTCCTAGAGGGTCATTG 540
QY 541 TCAAGAAACAAATGCTCAAGTATTGTTATTACCTACTTTTGGCAAGCTCAAAATGTGCAG 600
Db 541 TCAAGAAACAAATGCTCAAGTATTGTTATTACCTACTTTTGGCAAGCTCAAAATGTGCAG 600
QY 601 TTATTAATAATTAAGGATCGAGTTCAATATAAAGCACAAATGGTCCCAATTTTGGAGTCA 660
Db 601 TTATTAATAATTAAGGATCGAGTTCAATATAAAGCACAAATGGTCCCAATTTTGGAGTCA 660
QY 661 GAGNATGTAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTACCGGTGATATAC 720
Db 661 GAGNATGTAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTACCGGTGATATAC 720
QY 721 TATAGCGGATTAATAATGCAAAACGGCAGAGATATACCAATTAATGTTTATATGTTATCAG 780
Db 721 TATAGCGGATTAATAATGCAAAACGGCAGAGATATACCAATTAATGTTTATATGTTATCAG 780
QY 781 GTAGGTTTAAATCAGATATAAAGGGGGGACAGGTGCTGACACTTGGTTCGAAATTTAAT 840
Db 781 GTAGGTTTAAATCAGATATAAAGGGGGGACAGGTGCTGACACTTGGTTCGAAATTTAAT 840
QY 841 AAATTTCTGTAGAGATGACGTGGCGGTATTGGATATTATCGCTATATTTCCTCACTTAT 900
Db 841 AAATTTCTGTAGAGATGACGTGGCGGTATTGGATATTATCGCTATATTTCCTCACTTAT 900
QY 901 GATTTTGAGAAATATCCATTGGCCAAACACATGTAGAGTTGACCTAGGGAATTTTATACAGAT 960
Db 901 GATTTTGAGAAATATCCATTGGCCAAACACATGTAGAGTTGACCTAGGGAATTTTATACAGAT 960
QY 961 CGAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAAT 1020
Db 961 CGAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAAT 1020
QY 1021 GGGTTAGAGGCTAAATGGAACACGGGACCTGGTTTGTAGTTTACCTAGCAAAATAGGT 1080
Db 1021 GGGTTAGAGGCTAAATGGAACACGGGACCTGGTTTGTAGTTTACCTAGCAAAATAGGT 1080
QY 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGCTGGGTAGGAACTCGTCATTATGAA 1140
Db 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGCTGGGTAGGAACTCGTCATTATGAA 1140
QY 1141 GACTACACAAAGGGTAACGGTATTTTTCACACGTATGCTGGAACCTACGAGTAATGATCTA 1200
Db 1141 GACTACACAAAGGGTAACGGTATTTTTCACACGTATGCTGGAACCTACGAGTAATGATCTA 1200
QY 1201 CGTATATTGATTTTCAGAAATCCGATGTATATAAATTTACTTCAATAGCTATCATGAC 1260
Db 1201 CGTATATTGATTTTCAGAAATCCGATGTATATAAATTTACTTCAATAGCTATCATGAC 1260
QY 1261 CTAGTAGGAGAGACTACCGCTAGACACAGAGTATCGTGTGTTTCAAGGCGAGATTTTCGTAG 1320
Db 1261 CTAGTAGGAGAGACTACCGCTAGACACAGAGTATCGTGTGTTTCAAGGCGAGATTTTCGTAG 1320

QY 1321 GTAGGGGACCTGATTTAAATTTATGATGCAAGTAAATAATGGGCTAAGCAGAGATGACAATT 1380
Db 1321 GTAGGGGACCTGATTTAAATTTATGATGCAAGTAAATAATGGGCTAAGCAGAGATGACAATT 1380
QY 1381 GAACTAGCTTCCCACTTTGTATTCGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440
Db 1381 GAACTAGCTTCCCACTTTGTATTCGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440
QY 1441 TCAAAATCGGCATGTGTTGTATATGGAATCTCCAGAGTTAACTGATATATGGTTGGACACAT 1500
Db 1441 TCAAAATCGGCATGTGTTGTATATGGAATCTCCAGAGTTAACTGATATATGGTTGGACACAT 1500
QY 1501 ACAAGTTTAAACCGTGAATAATTAATGAAGCCAAATCAAAATTAACAATAACCCGCGGTG 1560
Db 1501 ACAAGTTTAAACCGTGAATAATTAATGAAGCCAAATCAAAATTAACAATAACCCGCGGTG 1560
QY 1561 AAGAGTTTATACCTTCAAAATTTATCTGCTAATGCTTATACCTATGTTAATAAAGGCACT 1620
Db 1561 AAGAGTTTATACCTTCAAAATTTATCTGCTAATGCTTATACCTATGTTAATAAAGGCACT 1620
QY 1621 CATACAGGTGGGATTTAATCCGTTTTTAAAGAACAAATCAGAGTATAAAGCAGTTTAT 1680
Db 1621 CATACAGGTGGGATTTAATCCGTTTTTAAAGAACAAATCAGAGTATAAAGCAGTTTAT 1680
QY 1681 GCAGGTGGCGAATTTAGATTTAATTAATAACAAAACTGCAGGACAAAGTTACCGTATT 1740
Db 1681 GCAGGTGGCGAATTTAGATTTAATTAATAACAAAACTGCAGGACAAAGTTACCGTATT 1740
QY 1741 CGTTTTCTGATGTCGACAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
Db 1741 CGTTTTCTGATGTCGACAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
QY 1801 TGGGTTTCAAAATCGTTTTGTATCGCTTCAAAAAATCTTACTCTGGAATTTATGACGATTTA 1860
Db 1801 TGGGTTTCAAAATCGTTTTGTATCGCTTCAAAAAATCTTACTCTGGAATTTATGACGATTTA 1860
QY 1861 AAATATAGTATTTTAAATTCGCTGAAATTTATCACACCTCCATTAACCTAGTTCAAAACATT 1920
Db 1861 AAATATAGTATTTTAAATTCGCTGAAATTTATCACACCTCCATTAACCTAGTTCAAAACATT 1920
QY 1921 CAGATGGATGTCGAGATGCAAGCGAATAGTTTTCATCAGATGTAAGCTGTTCTCGAC 1980
Db 1921 CAGATGGATGTCGAGATGCAAGCGAATAGTTTTCATCAGATGTAAGCTGTTCTCGAC 1980
QY 1981 AAAATTGAATTCCTCCCAAGTAATAACAACACTTTTGAATATGAGGAGAACGGGACCTTA 2040
Db 1981 AAAATTGAATTCCTCCCAAGTAATAACAACACTTTTGAATATGAGGAGAACGGGACCTTA 2040
QY 2041 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTAA 2082
Db 2041 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTAA 2082

RESULT 2

US-10-781-979-1
; Sequence 1, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1									
; LENGTH: 5980									
; TYPE: DNA									
; ORGANISM: Bacillus thuringiensis									
US-10-781-979-1									
Query Match									
Best Local Similarity 100.0%; Score 2082; DB 8; Length 5980;									
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GTGAAAAGATGATGTCATATCAAAATATAAATAAATGAATATGAATATGGAATCCTCATCG	60						
DB	168	GTGAAAAGATGATGTCATATCAAAATATAAATAAATGAATATGAATATGGAATCCTCATCG	227						
QY	61	AATAACACAATAACGCCAAACAGATATCCTTTTGGCAAATAATCGCGATATGCTACTATG	120						
DB	228	AATAACACAATAACGCCAAACAGATATCCTTTTGGCAAATAATCGCGATATGCTACTATG	287						
QY	121	TCTTGGAAATGATGTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATA	180						
DB	288	TCTTGGAAATGATGTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATA	347						
QY	181	ACAAGTATGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGAATTAAT	240						
DB	348	ACAAGTATGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGAATTAAT	407						
QY	241	ACACTATTATCAATAATAGGAAACCTAAATTCGACTAATCGTCAAACTGTGTGAGCAGCTT	300						
DB	408	ACACTATTATCAATAATAGGAAACCTAAATTCGACTAATCGTCAAACTGTGTGAGCAGCTT	467						
QY	301	TCTATATGTGATTTATTTCTATAATTCGTTAAAGAGGTAGCCGATAGTGTTTAAAGTGAT	360						
DB	468	TCTATATGTGATTTATTTATCTATAATTCGTTAAAGAGGTAGCCGATAGTGTTTAAAGTGAT	527						
QY	361	GGGATTCGAGATTTTTCAGCGTAAATTTGAAATAATATAGAGATATTAATCTTTCTATCTT	420						
DB	528	GGGATTCGAGATTTTTCAGCGTAAATTTGAAATAATATAGAGATATTAATCTTTCTATCTT	587						
QY	421	GGGGCTTTGGCTTAAAGACGTAACCACTTCAAAACGACAAATAATCTGATATCGGACAA	480						
DB	588	GGGGCTTTGGCTTAAAGACGTAACCACTTCAAAACGACAAATAATCTGATATCGGACAA	647						
QY	481	TTAGTTTATTTATTTTAAACTTTTTCAGAAAGAGATTTTCAATGAAATCTTAGGAGGTCATTTG	540						
DB	648	TTAGTTTATTTATTTTAAACTTTTTCAGAAAGAGATTTTCAATGAAATCTTAGGAGGTCATTTG	707						
QY	541	TCAGAAACAAATGCTCAAGTATTTGTTATTAATCTTCTTTTGCAGAGCTGAAATGTCAG	600						
DB	708	TCAGAAACAAATGCTCAAGTATTTGTTATTAATCTTCTTTTGCAGAGCTGAAATGTCAG	767						
QY	601	TTATTTACTATTAAAGGATGCGATTCATATAAGCACAAATGTTCCCATTTTGTAGTGCA	660						
DB	768	TTATTTACTATTAAAGGATGCGATTCATATAAGCACAAATGTTCCCATTTTGTAGTGCA	827						
QY	661	GAGAATGTAAGATCGGAATTAATATATCACTTAACAGTGGTTGTGATTTTACCGGTGATTAC	720						
DB	828	GAGAATGTAAGATCGGAATTAATATATCACTTAACAGTGGTTGTGATTTTACCGGTGATTAC	887						
QY	721	TATAGCGAATTAATAATGCAAAACGGCAGAGATATCAATATTTGTTTATTTAGTTATCAG	780						
DB	888	TATAGCGAATTAATAATGCAAAACGGCAGAGATATCAATATTTGTTTATTTAGTTATCAG	947						
QY	781	GTAGGTTTAAATCAGATATAACAGGGGGGACAGGTGCTGACATTTGGTCGAAATTTAAT	840						
DB	948	GTAGGTTTAAATCAGATATAACAGGGGGGACAGGTGCTGACATTTGGTCGAAATTTAAT	1007						
QY	841	AAATTTTCGTAGAAATGACGTTGGCGGTATTTGGATTTATTCGTATATTTTCCAACTTAT	900						
DB	1008	AAATTTTCGTAGAAATGACGTTGGCGGTATTTGGATTTATTCGTATATTTTCCAACTTAT	1067						
QY	901	GATTTTGAGAAATATCCATTGCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT	960						
DB	1068	GATTTTGAGAAATATCCATTGCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT	1127						
QY	961	GCAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAATTTGGCTTAATCTTTTAAT	1020						
DB	1128	GCAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAATTTGGCTTAATCTTTTAAT	1187						
QY	1021	GGGTTAGAGGCTAATGGAAACACGGGACCTGGTTTATAGTTTACCTTGGCTTAGCAAAATAGGT	1080						
DB	1188	GGGTTAGAGGCTAATGGAAACACGGGACCTGGTTTATAGTTTACCTTGGCTTAGCAAAATAGGT	1247						
QY	1081	ATATATAATGAGTATGTTTCGAGATATTTTTCGGGCTGGGTAGGAACTGCTCATTTATGAA	1140						
DB	1248	ATATATAATGAGTATGTTTCGAGATATTTTTCGGGCTGGGTAGGAACTGCTCATTTATGAA	1307						
QY	1141	GACTACACAAAAGGTAACGSTATTTTCAACGATGCTCTGGGAACCTACGAGTATGATCTA	1200						
DB	1308	GACTACACAAAAGGTAACGSTATTTTCAACGATGCTCTGGGAACCTACGAGTATGATCTA	1367						
QY	1201	CGTAATATTGATTTTTCAGAAATCCGATGTATATAAAATTTACTTTCATTAGCTATCATGAAC	1260						
DB	1368	CGTAATATTGATTTTTCAGAAATCCGATGTATATAAAATTTACTTTCATTAGCTATCATGAAC	1427						
QY	1261	CTAGTAGGAGAGACTACCCCTAGACCCAGAGTATCGTGTGTTTCAAAAGCAGATTTTTCGTAGG	1320						
DB	1428	CTAGTAGGAGAGACTACCCCTAGACCCAGAGTATCGTGTGTTTCAAAAGCAGATTTTTCGTAGG	1487						
QY	1321	GTAGGGGGACCTGATTTTAAATTTATGATGCAGGTAAATAATGGGCTAAGCAGGATGACAAAT	1380						
DB	1488	GTAGGGGGACCTGATTTTAAATTTATGATGCAGGTAAATAATGGGCTAAGCAGGATGACAAAT	1547						
QY	1381	GAATCTACGTTCCCACTTGTATTTGCACTCTAATGGTGTGTAGAGGACCTCTCATAGATTAA	1440						
DB	1548	GAATCTACGTTCCCACTTGTATTTGCACTCTAATGGTGTGTAGAGGACCTCTCATAGATTAA	1607						
QY	1441	TCAAATTCGGGATGTGTTATATGGAATCTCCAGAGTTAAACGTATATGGTTGGACACAT	1500						
DB	1608	TCAAATTCGGGATGTGTTATATGGAATCTCCAGAGTTAAACGTATATGGTTGGACACAT	1667						
QY	1501	ACAAGTTTAAACGTAATAATTAATGAAGCCAAATCAAAATTTACACAAATACCGCGGGTG	1560						
DB	1668	ACAAGTTTAAACGTAATAATTAATGAAGCCAAATCAAAATTTACACAAATACCGCGGGTG	1727						
QY	1561	AAGAGTTATTTACCTTTCAAAATTTATCTGTCTAATGCTTATACCTATGTATAAAGGCACCT	1620						
DB	1728	AAGAGTTATTTACCTTTCAAAATTTATCTGTCTAATGCTTATACCTATGTATAAAGGCACCT	1787						
QY	1621	CATACAGGTGGGATTTAATTCGGTTTTTAAAGAAACAAATTCAGAGTATTAACGAGTTTAT	1680						
DB	1788	CATACAGGTGGGATTTAATTCGGTTTTTAAAGAAACAAATTCAGAGTATTAACGAGTTTAT	1847						
QY	1681	GCAGGTGGCGGAATTTAGATTGATTATTAATACAAACCTGCAGGACAAAGTTACCGTATT	1740						
DB	1848	GCAGGTGGCGGAATTTAGATTGATTATTAATACAAACCTGCAGGACAAAGTTACCGTATT	1907						
QY	1741	CGTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTTAGTGTATATCTTTATCCAGAGGT	1800						
DB	1908	CGTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTTAGTGTATATCTTTATCCAGAGGT	1967						
QY	1801	TGGGGTTCAAATTCGTTTTGTATCGCTTGAATAATCTTACTCTGGAAATTTATGACGATTTA	1860						
DB	1968	TGGGGTTCAAATTCGTTTTGTATCGCTTGAATAATCTTACTCTGGAAATTTATGACGATTTA	2027						
QY	1861	AAATATAGTGAATTTTAAATTCGTCGAAATTTATCACCTCCATTTACCTAGTTTCAACATTT	1920						
DB	2028	AAATATAGTGAATTTTAAATTCGTCGAAATTTATCACCTCCATTTACCTAGTTTCAACATTT	2087						
QY	1921	CAGATGGATGTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGCTGCTTCGAC	1980						
DB	2088	CAGATGGATGTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGCTGCTTCGAC	2147						
QY	1981	AAATTTGAATTCCTCCCAAGTAAATCAACAACTTTTAGAATATGAGGGAGAAACGGACCTTA	2040						
DB	2148	AAATTTGAATTCCTCCCAAGTAAATCAACAACTTTTAGAATATGAGGGAGAAACGGACCTTA	2207						

QY 2041 GAAAAACAAAGACGCGGTGAACGATCTGTTTACCAATTA 2082
Db |||||||

QY 2208 GAAAAACAAAGACGCGGTGAACGATCTGTTTACCAATTA 2249
Db |||||||

RESULT 3

US-10-781-979-4
; Sequence 4, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2073)

US-10-781-979-4

Query Match 99.6%; Score 2073; DB 8; Length 2073;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGAGTCATATCAAAATAAATGAATGAAATATTGGAATCTCATCGAATAACACA 69
Db 1 ATGAGTCATATCAAAATAAATGAATGAAATATTGGAATCTCATCGAATAACACA 60

QY 70 AATACGCCAAACAGATATCTTTTCCAAATATCGGATATCTACTATGCTTGGAAAT 129
Db 61 AATACGCCAAACAGATATCTTTTCCAAATATCGGATATCTACTATGCTTGGAAAT 120

QY 130 GATTGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 189
Db 121 GATTGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 180

QY 190 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGGAATTAATACATATTA 249
Db 181 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGGAATTAATACATATTA 240

QY 250 TCAATAATAGGAATACTAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTATCGGATGCA 309
Db 241 TCAATAATAGGAATACTAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTATCGGATGCA 300

QY 310 GATTATTATCTATAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTATCGGATGCA 369
Db 301 GATTATTATCTATAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTATCGGATGCA 360

QY 370 GATTGTCAGGTAATTTGAAATATATAGAGAGTATATCTTTCTTATCTCGGGCTTGG 429
Db 361 GATTGTCAGGTAATTTGAAATATATAGAGAGTATATCTTTCTTATCTCGGGCTTGG 420

QY 430 CTTAAAGCGGTAAACCACTTCAAAAGCAAAATATCTGATATCGGAAATAGTTTAT 489
Db 421 CTTAAAGCGGTAAACCACTTCAAAAGCAAAATATCTGATATCGGAAATAGTTTAT 480

QY 490 TATTTTAAATCTTCAGAAAGAGATTTCAATGAAATTTCTAGAGGGGTCAATGTCAGAAAC 549
Db 481 TATTTTAAATCTTCAGAAAGAGATTTCAATGAAATTTCTAGAGGGGTCAATGTCAGAAAC 540

QY 550 AATGCTCAAGTATTGTTTATTACCTACTTTTGCACAAAGCTCAAAATGTCAGTATTACTA 609
Db |||||||

QY 610 TTAAGGATGAGTTCATATATAAAGCAAAATGTTTCCCATTTTTCAGTGCAGAGATGTA 669
Db |||||||

QY 670 AGATCGGAATTAATATACCTAAACAGTGGTGTGATTTTACCGGTGATTAATCATAGGGA 729
Db |||||||

QY 730 TTAANAATGCAAAACGCGAGAGTATACCAATTTATTGTTTATATTTGTTATCGTATCAGTATGTTA 789
Db |||||||

QY 790 AATCAGATATAAAGAGGGGGGACAGGTCTGCACACTTGGTTCGAAATTTAAATAAATTCGT 849
Db |||||||

QY 850 AGAGAAATGACGTTGGCGGTATTGGATATATCGCTATATTTCCAACTTATGATTTGAG 909
Db |||||||

QY 910 AAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTATACAGATCGAGTGGGA 969
Db |||||||

QY 970 TATTCATCGGAACTTATAGTTGGTTACGGAATTTGGCTTAATCTTTTAAATGGGTAGAG 1029
Db |||||||

QY 1030 GCTAATGGAACACGCGGACCTGGTTTGTGTTACTTTGGCTTAGCAAAATAGGTATATAAT 1089
Db |||||||

QY 1090 GAGTATGTTTCGAGATATTTTCCGGCTGGGTAGGAACCTCGTCAATATGAGAGACTACACA 1149
Db |||||||

QY 1150 AAGGTAACGTTATTTTCAACGATGTCTCGAACTACGAGTAATGATCTACGTAATATT 1209
Db |||||||

QY 1210 GATTTCAGAAATCCGATGTATATAAAATTTACTTTTATTAGCTATCATGAACCTAGTAGGA 1269
Db |||||||

QY 1270 GAGACTACCGCTAGACAGAGTATCGTGTTCGTTTCAAGGCGAGATTTTCGTAGGGTAGGGGA 1329
Db |||||||

QY 1330 CCTGATTTAAATTTATGATGAGGTAAATAATCGGCTTAAGCAGGATGACAAATTTGAATCTACG 1389
Db |||||||

QY 1390 TTCCCACTTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTTCAATGCG 1449
Db |||||||

QY 1450 GCATGTGTTGATATGGAACCTCCAGAGTTAAAGTATATGTTTGGACACATACAAGTTTA 1509
Db |||||||

QY 1510 AAAAGTGAATAATAATTTGAAGCCAAATTAACAAATTAACAAATTAACAAATTAACAAATTAACAAATTA 1569
Db |||||||

QY 1570 TACCTTCAAAATTTATCTTGTAAATGCCTTATACCTATGTAATAAAGGCACTCATACAGGT 1629
Db |||||||

QY 1630 GGGGATTTAATCCGTTTTTTTAAAGAAACAAATACAGATATAACGCGAGTTTATGTCAGGTGGC 1689

Db 1621 GGGGATTAATCCGTTTTTAAAGAACAAAATCAGAGTATAACGAGTTTATGCGAGTGGC 1680
Qy 1690 GGAATTAGATTGATTATTAATAACAAAACGCGAGGACAAAGTTTACCGTATTTCGTTTCGT 1749
Db 1681 GGAATTAGATTGATTATTAATAACAAAACGCGAGGACAAAGTTTACCGTATTTCGTTTCGT 1740
Qy 1750 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGTTGGGGTTCA 1809
Db 1741 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGTTGGGGTTCA 1800
Qy 1810 AATCGTTTCTATCGCTTGA AAAATCTTACTCTGGA AATTATGACGATTTAA AATATAGT 1869
Db 1801 AATCGTTTCTATCGCTTGA AAAATCTTACTCTGGA AATTATGACGATTTAA AATATAGT 1860
Qy 1870 GATTTTAAATTCGCTGA AATTTATCACACCTCCATTTACCTAGTTTCA AATTTCA AATTTGAA 1989
Db 1861 GATTTTAAATTCGCTGA AATTTATCACACCTCCATTTACCTAGTTTCA AATTTCA AATTTGAA 1980
Qy 1930 GTGGAGATCAAGCGAATAGTTTTC AATCAGATGTAAACGTGTTCTCGA CAAAATTTGAA 2049
Db 1921 GTGGAGATCAAGCGAATAGTTTTC AATCAGATGTAAACGTGTTCTCGA CAAAATTTGAA 1980
Qy 1990 TTCTCCCAAGTAAATACAACTTTTGA AATATGAGGAGAAACGGACCTAGAAAAAACA 2049
Db 1981 TTCTCCCAAGTAAATACAACTTTTGA AATATGAGGAGAAACGGACCTAGAAAAAACA 2040
Qy 2050 AAGAACGCGTGAACGATCTGTTTACCAATTA 2082
Db 2041 AAGAACGCGTGAACGATCTGTTTACCAATTA 2073

RESULT 4

US-10-782-141-2
; Sequence 2, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargies, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(2019)
US-10-782-141-2

Query Match 35.9%; Score 747.2; DB 8; Length 2019;
Best Local Similarity 69.8%; Pred. No. 4e-160;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;
Qy 1 GTGAAAAGATGAGTCCATATCAAAAATAAATGAATATGAATATGGAATCCTCATCG 60
Db 1 GTGAAAATATGAATTTCTTATCAAAAATACAAAATGAATATGAATATGGAATCCTCATCG 60
Qy 61 AATAACAAAAATACGCCAACAGATATCTTTTGGCAAAATACCGGATATGCTACTATG 120
Db 61 AATAACAAAAATATGTCAAACAGATATCTTTTGGCAAAATACCGGATATGCTACTATG 120
Qy 121 TCTTGAATGATTGTTCAGGGAATCTCATGGGAATTTTGGGAATCAGTCGAAACGATA 180

Db 121 AACCTGCAGCGTTGTTCAGGGAAGGCCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 180
Qy 181 ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTTAGTTGGGTGGAATTAAT 240
Db 181 GTAACTATTGGGACATACCTTATACAAATCTTGTCTAGAACCCCGGTATAGGTGGAATTCCT 240
Qy 241 ACACTATTATCAATAATAGGAAAACCTAAATCCGACTAAATCGTCAAACTGTGTGTCAGACATT 300
Db 241 GTAAATATTTCAATATAAACAACCTCATCTCGTCTTCTGGTCAATCTGTGGGACGACATT 300
Qy 301 TCTATATGATGATTTATTTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAGTGAT 360
Db 301 TCTATATGATGATTTATTTAGTATCTATAATTTCTGTAAAGAGGTAGACGAGAGCGTGTTAAGTGAC 360
Qy 361 GCGATTGCGAGATTTTACCGGTAAATTTGAAAATATTATAGAGATTAATTTCTTCTTATCTT 420
Db 361 GGGGTTGCGAGATTTTGGAGGTTGAAAATGACTGCTTTATCAAGATTTATTTATCTTCAATTATCTT 420
Qy 421 GGGGCTTGGCTTAAAGACGCTAAACCCACTTTCAAAAGACAAAATAATTTCTGATATCGGACAA 480
Db 421 GAGGATTGGCTTACAG-----ATAATCAATCTTAAAAAATCTTGTGTGAC 465
Qy 481 TTAGTTTATTTATTTTAAACTTTTCAAGAAAGAGATTTTCAATGAAATTTCTAGGAGGTCATTG 540
Db 466 GTAGTTTAAACAGTTTCAAGCACGCGGAAGAAGATTTTCACTAACTTTTAGCAGGTCATTGA 525
Qy 541 TCAAGAAACAATGCTCAAGTATTTGTTATTTACCTACTTTTGGCAACAGCTGCAAAATGTCAG 600
Db 526 TCAAGACAGAAAAGCTGAAAATATTTATTTGCGCTACGTATGTGCAAGCTGCAAAATGTCAT 585
Qy 601 TTATTACTATTAGGGATGCGAGTTCAATATAAAGCACAAATGTTCCCATTTTGTAGTGCA 660
Db 586 TTATTACTATTAGGGACCGCAGTTAAATATAAAGAAATGGGACAGTAGTGTCTCCACCG 645
Qy 661 GAGAATGTAAAGATCGGAATTAATATCACCTAACAGTGGTTGTGATTTTACCGGTGATTAC 720
Db 646 TTGTATCCAGGTCAGGAGAA-----CTGATTGT 675
Qy 721 TATGAGCGATTTAAATGCAAAACGGGACGAGATATACCAATTTATTTTATATTGTTATCAG 780
Db 676 AACGAGCGGTTAAAGACGAAAAATAAAGAGATGATCTAATTTATTTGTAGGTTGTTAATAC 735
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGACAGGTGCTGACACTTTGGTCGAAATTTAAT 840
Db 736 AAGGTTTATAGATCAGATAAGACAGCGGGTACAGTCTGAAAGTTTGGTCGAAATTTAAT 795
Qy 841 AAATTTCTGTAGAGAAATGACGTTGGCGTATTGGATATTATCGCTATATTTCCTCAACTAT 900
Db 796 AAATTTCTGTAGAGAAATGACGTTGGCGTATTGGATATTATTTGCTATATTTCCTCAACTAT 855
Qy 901 GATTTTGAAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTATACAGAT 960
Db 856 GATTTTGAAGAAATATCCATTTAGCAACAAGTGTAGAGTTAACTAGGGAATTTATACAGAT 915
Qy 961 GCAGTGGGATATTTCATCGGGAATTTATAGTTGGTTACGGAATTTGGCCTAATACTTTAAT 1020
Db 916 CCAGTGGGATATTTCAGGGGGAATTTATGGTTGGGAACCGTTTTT-----TTAGCTTTAAT 969
Qy 1021 GGGTTAGAGGCTAATGGAACACCGGACCTGGTTTTAGTTTACTTTGGCTTAGCAAAAATAGGT 1080
Db 970 TCGGTAGAGCAAAATGGAACACCGGACCTGGTTTGTACTTTGGCTTCAAGCTATAGAT 1029
Qy 1081 ATATATAATAGATGATGTT-----TCGAGATATTTTGGCGGTGGGTAGGAACTCGT 1131
Db 1030 ATATATAGTCAATCTTATTAATCTTCAGCTTGGTTATCTTAGTGGCTGGGGGGAACCTCGT 1089
Qy 1132 CATTATGAGACTACACAAAGGTAAACGTTATTTTCAACGTATCTCTGGAATACGAGT 1191
Db 1090 CATTATGAGACTTCAACAAAGGTAAACGTTGCTTTTCAACGTATCTCTGGAATACGAGT 1149
Qy 1192 AATGATCTACGTAATATTGATTTTTCAGGAATGCGGATGTATATAAAAATTTACTTTTAGCT 1251

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Db 1150 AATAATCCAGTAATAATTATTTTGGCAATACCGATATATTATAAATATTATTTCAATTAGCT 1209
QY 1252 A---TCATGAACCTAGTAGGAGAGACTACCGGTAGACCAAGATATCGTGTTCCTCAAGGCA 1308
Db 1210 AGATATGCAATGCAACCGTTTGTGGGTATTCAATCCACCGCATCTTGTTCACGTGCA 1269
QY 1309 GATTTCCTGAGGTAGGGGACCTGATTTAAATATTATGATGCAGGTAAATATGGCTAAGC 1368
Db 1270 GAATTTTTCCGACACACTAAATACCTTCCTGTATGAGGTAAACAGTTCTCGG---TAC 1326
QY 1369 AGGATGACAATGAATCTACGTTCCCACTTGT-----ATTGCACCTCTAATGGTGTAGA 1422
Db 1327 TCACAGACAATGAATCTGTGTACCAAGGTATTATAAAGATCTACCACCTAGTCGTACA 1386
QY 1423 GGACCTCTCATAGATTATCAAAATGCGGCATGTGTGTATATGGAACCTCCAGAGTTAC 1482
Db 1387 AATTACTCTCATAGATTATCAAAATGCGGCATGTGTTCAAAATGAAACCTCCAGAGTTAC 1446
QY 1483 GTATATGGTTGACACATCAAGTTTAAACGTGAATATATAATTTGAAGCCATCAATTT 1542
Db 1447 GTATTGGTTGACACATCAAGTATGAAAAAAGATTAATCGAATTTATCCAGATAAAATTT 1506
QY 1543 ACACAAATACCGCGGTGAAGTTATTACCTTCAAAATTTCTTGCTAATGCTATACC 1602
Db 1507 ACGCAATTCCTGCAGTAAAGCTTTTGGCCTACCAGCAGGTACAGGATATGCGAGGT 1566
QY 1603 TAGTAATAAAGGCACT 1620
Db 1567 TAGGTCACAGCTGGGCGCT 1584
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RESULT 5

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US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: A Delta-Endotoxin Gene and
; METHODS FOR ITS USE
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-141-1
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Query Match 35.9%; Score 747.2; DB 8; Length 2145;
Best Local Similarity 69.8%; Pred. No. 4.1e-160;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;
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QY 1 GTGAAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCTCTCATCG 60
Db 127 GTGAAAAATATGAATCTTTATCAAAATACAAATGAATATGAATATTTCTGGATGGTTCCCG 186
QY 61 AATAACAAAAACGCCAACAGATATCTTTTGGCAATAAATCGGGATATGCTACTATG 120
Db 187 AATAACAAAAATATGTCAACAGATATCTTTTGGCAAGATCCAAATATATTTCTAT 246
QY 121 TCTTGGATGATGTGACGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAACGATA 180
Db 247 AACCTGGACGCTTGTGAGGGAAGGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATA 306
QY 181 ACAAGTATTTGGGATAAATCTTATAGATTTTGTATAGAACCTAGTTTGGGTGGAATTAAT 240
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Db 307 GTAACATTTGGGACATACCTTTATACAAATTTGCTAGAACCCGGTATAGGTGGAATTCCT 366
QY 241 ACACATTTATCAATAATAGGAAACTAATTCGACATAATCGTCAAACTGTGTGACACATTT 300
Db 367 GTAATATTTTCAATATATAAACAACCTCATTCGGTCTTCTGGTCAATCTGTGGCAGCAT 426
QY 301 TCTATATGTGATTTATATCTATTAATTCGTAAAGAGGTAGCCGATAGTGTGTTTTAAGTGA 360
Db 427 TCTATATGTGATTTAGTATCTATAATTCGTAAAGAGGTAGACGAGCGGTGTAAAGTGAC 486
QY 361 GCGATTGACAGATTTTGACGGTAAATTTGAAATATATAGAGATATTTCTTTCTTATCTT 420
Db 487 GGGGTGACAGATTTTGGGGTGAATGACTGCTTATCAAGATTTATCTTCAATTTATCTT 546
QY 421 GGGGCTTCGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTCGATATCGGACAA 480
Db 547 GAGGATTCGCTTACAG-----ATAAATCAAAATCTTAAAAAACCTTGTCTGAC 591
QY 481 TTAGTTTATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTTAGGAGGGTCATGT 540
Db 592 GTAGTTAAACAGTTTCCAAAGCAGCGGAAGAGATTTCACTAAACCTTTTAGCAGGGTCA 651
QY 541 TCAAGAAACATGCTCAAGTATTTGTTATCTACTTTTGCACAGCTGCAAAATGTCGAG 600
Db 652 TCAAGACAGAAAGCTGAAATATTTATTTGCTACGTATGTGCAAGCTGCAAAATGTGAT 711
QY 601 TTATTACTATTAAAGGATGCAGTTCAATATATAAGCACAATGTTGCCATTTTGTAGTGCA 660
Db 712 TTATTACTATTAAAGGACGAGTTAAATATATAAAGATATGGGACTAGTGTGTCACCG 771
QY 661 GAGAAATGAGATCGGAATTAATATCACTAACAGTGGTGTGTGATTTTACCGGTGATTAAC 720
Db 772 TTGTATCCAGGTCAGGGAGAA-----CTGATTTGT 801
QY 721 TATGAGCATTTAAATGCAAAACGCGCAGAGTATACCAATTTATTTTATATTTGTTATCAG 780
Db 802 AACGAGCGGTTAAAGCGGAAATATAAGAGATATCTAATTTATTTGTTAGGGTGGTATAC 861
QY 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTCTGCACACTTGTGCGAAATTTAAT 840
Db 862 AAGGTTTATGATCAGATTAAGACAGCGGGTACAGTCTGGAAGTTTGTTCGAAATTTAAT 921
QY 841 AAATTTCTAGAGAAATGACCTTGGCGGTATTTGATATTTATCGCTATATTTTCCAACTTAT 900
Db 922 AAATTTCTAGAGAAATGACCTTGGCGGTATTTGATATTTATTTGCTATATTTTCCAACTTAT 981
QY 901 GATTTTGAGAAATATCCATTCGCCACACATCTAGAGTTGACTAGGGAATTTATACAGAT 960
Db 982 GATTTTGAATAATATCCAAATAGCAACAGTGTAGAGTTAACTAGGGAATTTATACAGAT 1041
QY 961 GCAGTGGGATATTTCATCGGAACTTATAGTTGGTTACGGAATTTGGCCTTAATCTTTTAA 1020
Db 1042 CCAGTGGGATATTTCAGGGGAAATTTATGTTTGGGAACGGTTTT-----TTAGCTTTAAT 1095
QY 1021 GGGTTAGAGGCTAATGGAACACCGGGACCTGGTTTGTAGTTACTTGGCTTAGCAAAATAGGT 1080
Db 1096 TCGGTAGAAGCAAAATGGAACACCGGGACCTGGTTTGTAGTTACTTGGCTTCAAGCTATAGAT 1155
QY 1081 ATATATATGAGTATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGACTCGT 1131
Db 1156 ATATATGTCATTTCTTAAATCTTCAGCTTGGTTATCTTAGTGGCTGGGGGGAACTCGT 1215
QY 1132 CATTATGAAGACTACACAAAGGGTAAACGGTATTTTCAACGTATGTCTGGAACCTACGAGT 1191
Db 1216 CATTATGAAGACTTCAAAAGGGTAAACGGTCTTTTCAACGTATGTCTGGAACCTACGAGT 1275
QY 1192 AATGATCTACGTAATTTGATTTTTCAGAAATGCCGATGTATATAAATTTACTTTCAATAGCT 1251
Db 1276 AATAATCCACGTAATTTATTTTGGCAATACCCGATATATTTTAAATTTATTTTCAATAGCT 1335
QY 1252 A---TCATGAACCTAGTAGGAGAGACTTACCCCTAGACCAGAGATATCGTGTGTTTCAAGGCA 1308
```

Db 1336 AGATATGCAATGCAACCGGTTGTTGGGTATTCATCCACGGCATCTTGTTCACGTGCA 1395
QY 1309 GATTTTCGTAGGTAGGGGACCTGATTTAAATATGATGTCAGGTAAATATGGCTAAGC 1368
Db 1396 GAATTTTTCGGAACAACACTAAATATCTTCTGTATGAGGTAAACAGTTCTTGGG---TAC 1452
QY 1369 AGGATGACAATTTGAATCTACGTTCCCACTTGT-----ATTGCACTCTAATGGTGTAGA 1422
Db 1453 TCACAGACAATTTGAATCTGTGTTACCAAGGTATTAATAAGGATCTACCACCTAGTCTGACA 1512
QY 1423 GGACCTCTCATAGATATCAAAATGCGGCGATGTTGTATATGGAACCTCCAGAGTTAAC 1482
Db 1513 AATTACTCTCATAGATATCAAAATGCGGCGATGTTTCAAAATGAAACCTCCAGAGTTAAC 1572
QY 1483 GTATATGTTGGACACATACAAGTTTAAACGTTGAAATATATTTCAAGCCCAATCAATTT 1542
Db 1573 GTATTTGTTGGACACATACAAGTATGAAATAAGATAATTCGAATTTATCCAGATAAATTT 1632
QY 1543 ACACAAAATACCGCGGTGAAGGTATTTACCTTCAAAATTTATCTTCTAATGCTTATACC 1602
Db 1633 ACGCAAAATTCCTGCACTAAAGCTTTTGCCTTACCAGCAGGTACAGGATATGACAGGAT 1692
QY 1603 TATGTAATTAAGGCACT 1620
Db 1693 TACGTACAGCTGGGCT 1710

RESULT 6

US-10-782-141-4
; Sequence 4, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR FILING DATE: 60/448,632
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
US-10-782-141-4

Query Match 35.5%; Score 739.8; DB 8; Length 2010;
Best Local Similarity 69.7%; Pred. No. 2e-158;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;
QY 10 ATGAGTCCATATCAAAATGAATATGAATATTTGGAATCTCTCATCGAATAACACA 69
Db 1 ATGAATTTCTTATCAAAATCAAAATGAATATGAATTTCTGATGGTTCCCGGAATAACACA 60
QY 70 AATACGCCAACAGATATCTTTTGGCAATATATCGGGATATGTCTACTATGCTTTGGAAAT 129
Db 61 AATATGTCAACAGATATCTTTTGGCAATATATTTGCAAGGATCCAAATATATTTCTTAAACCTGGAC 120
QY 130 GATTGTTCAGGAACTCTCATGGGATGAATTTTCGGAATCAGTCGMAACGATACAGATATT 189
Db 121 GCTTGTTCAGGAAAGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATAGTAATATT 180
QY 190 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATACACTATTA 249

Db 181 GGGACATACCTTTATACAAATCTTGTAGAACCCGGTATAGGTGGAATTCCTCTAATATTT 240
QY 250 TCAATAATAGGAAAACCTAATTCGCACTAATTCGTCAAACTGTGTACGACACTTTCTATATGT 309
Db 241 TCAATAATAAACAAACCTCAATTCGCTTCTGCTCAATTCGTGTGCGCAGCACTTTCTATATGT 300
QY 310 GATTTATTATCTAATTCGTAAAGAGGTAGCCGATAGTGTGTTTAAAGTACATGCGATTGCA 369
Db 301 GATTTAGTATCTAATTCGTAAAGAGGTAGACGAGAGCGGTGTTAAGTACGCGGGTTGCA 360
QY 370 GATTTTGACGCTAAATTTGAAAAATTTATAGAGAGTATTTATCTTTCTTATCTTGGGCTTG 429
Db 361 GATTTTGAGGGTGAATGACTCTTATCAAGATTTATTTCTTCAATTTATCTTCTGAGGATTCG 420
QY 430 CTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAAATAGTTTAT 489
Db 421 CTTACAG-----ATAAATCAAAATCTTAAAAAACTTGTCTACGCTAGTTTAA 465
QY 490 TATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCAATTTGTCAAGAAC 549
Db 466 CAGTTTCCAAAGCAGCGGAAGAGATTTTCACTAACTTTTACGAGGGTCAATTTCAAGACAG 525
QY 550 AATGCTCAAGTATTTGTTATTTACTACTTTTTCACAAGCTGCAAAATGTCAGTATTTACTA 609
Db 526 AAAGCTGAAATATTTATTTGCTAGCTATGTGCAAGCTGCAAAATGTCGATTTTACTA 585
QY 610 TTAAGGGATGCACTTCAATATATAAGCAATAGTGTCCCATTTTGTAGTCCAGAGATGTA 669
Db 586 TTAAGGGACGCAAGTTAAATATATAAAAGAAATGGGCACTAGTGTGTCCACCGTTGTATCCA 645
QY 670 AGATCGGAATTAATATATCACCTAACAGTGTGTGATTTTACCGGTGATTTACTATGAGCGA 729
Db 646 GGGTCAGGGAGAA-----CTGATTTGAACGAGCGG 675
QY 730 TTAATAATGCAAAACGCGCAGAGTATACCAATTTATTTGTTATATTTGGTATCAGGTAGTTTA 789
Db 676 TTAATAAGCGAAAATAAAAGAGTATTAATTTATTTGTAGGGTGGTATAAACAAGGGTTTA 735
QY 790 AATCAGATATAAACAGCGGGGCGAGCTGTGACACTTTGTCGAAATTTAATAAATTTCTGT 849
Db 736 GATCAGATAAGACAGCGCGGTAACAAGTGTGAAAGTTTGTGCGAAATTTAATAAATTTCTGT 795
QY 850 AGAGAAATGACGCTTCGCGGTATTTGATATTTATCGCTATATTTTCCAACTTTATGATTTGAG 909
Db 796 AGAGAAATGACGCTTCGCGGTATTTGATATTTATTTGCTATATTTTCCAACTTTATGATTTGAA 855
QY 910 AAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGATCAGGTGGGA 969
Db 856 AAATATCCATTTAGCAACAAGTGTAGAGTTAACTAGGGAAATTTATACAGATCCAGTGGGA 915
QY 970 TATTCATCGGAACTTTTAGTTGGTTACGGAATTCGCCCTAATACCTTTTAAATGGGTTAGAG 1029
Db 916 TATTCAGGGGGAATTTATGGTTGGGAACGGTTTT-----TTAGCTTTTAAATTCGGTAGAA 969
QY 1030 GCTAATGGAAACAGCGGGACCTGGTTTGTAGTTACTTCGCTTAGCAAAATAGGTATATATAAT 1089
Db 970 GCAATATGAAACAGCGGGACCTGGTTTGTAGTTACTTCGCTTCAAGCTATAGATATATATAGT 1029
QY 1090 GAGTATGTT-----TCGAGATATTTTTCGCGCTCGGTAGGAACTCGTCATTTATGAA 1140
Db 1030 CATTTCTATTATCTTTTCAGCTTGGTTTATCTTAGTGGCTGGGGGGAACCTGTCATTTAGAA 1089
QY 1141 GACTACACAAGGGTAAACGGTATTTTTCAAACGTATGTCTGGAACCTACGAGTAAATGATCTA 1200
Db 1090 GACTTTCACAAAGGGTAACGGTCTTTTCAACCGTATGTCTGGAACCTACGAGTAAATATCCA 1149
QY 1201 CGTATATTTGATTTTTCAGAAATCGCGATGTATATAAATTTACTTTCATTTAGCTA---TCATG 1257
Db 1150 CGTATATATTTTTCGCAATACCGATATATTTTAAATTTATTTTCAATTTAGCTAGATATGCA 1209
QY 1258 AACCTAGTAGGAGAGACTACCGCTAGACAGAGTATCGTGTGTTTCAAAGGCAAGTTTCTGT 1317
Db 1210 ATGCAACCGTTTGTGGGTATTTCAATCCACGGCATCTTGTTCACGTGCAGAAATTTT 1269

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QY 1318 AGGTAGGGGACCTGATTTAAATATGATGAGGTAAATAATGGGCTAAGCAGGATGACA 1377
Db 1270 CCGCAACACTAAATACTTCTCTGATGAGGTAACAGTCTCTGGG---TACTCACAGACA 1326
QY 1378 ATTGAATCTACCTCCACTTGT-----ATTGCACCTCTAATGGTGTAGAGGCCCTCT 1431
Db 1327 ATTGAATCTGTGTACCAGGTATTAATAAGGATCTACCACCTAGTCGTACAAATTACTCT 1386
QY 1432 CATAGATATCAAAATCGGCGATGTGTGTATATGGAATCTCCAGAGTTAAACGTATATGCT 1491
Db 1387 CATAGATATCAAAATCGGCGATGTGTCAAAATGAACCTCCAGAGTTAAACGTATTTGT 1446
QY 1492 TGGACACATCAAGTTTAAACGTAATAATAATGAAGCAATCAAAATTAACAATA 1551
Db 1447 TGGACACATCAAGTATGAATAAAGATATCGAATTTATCCAGATAAAATTAACGCAATT 1506
QY 1552 CCGGCGGTGAAGGTTATTAACCTTCAAAATTAATCTTGCTTAATGCCTATACCTATGTA 1611
Db 1507 CTGCGAGTAAAGCTTTTGGCCCTACCAGCGGTACAGGATATGCGAGGTTACGTCACA 1566
QY 1612 AAAGGCACT 1620
Db 1567 GCTGGCGCT 1575
```

RESULT 7

```
US-10-099-285-71
; Sequence 71, Application US/10099285
; Publication No. US20030105319A1
```

GENERAL INFORMATION:

APPLICANT: Schnepf, H. Ernest

Wicker, Carol

Narva, Kenneth E.

Walz, Michelle

Stockhoff, Brian

Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285

FILING DATE: 15-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/002,285

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/886,615

FILING DATE: 1-JUL-1997

APPLICATION NUMBER: US 08/674,002

FILING DATE: 1-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 3471 base pairs

TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285-71
```

Query Match 8.1%; Score 168.6; DB 5; Length 3471;

Best Local Similarity 52.5%; Pred. No. 1e-27;

Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

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QY 156 AATTGGGAATCAGTCGAAACGATAACAAAGTATTGGGATAAATCTTATAGAGTTTGTGAT 215
Db 153 AATAGGCGATCGACGAAAAGAGCAGTATCTATTGGGACAACCATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGANAACATAAT 269
Db 213 AGCACCTTCTTACTTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACTGTGTCAGCACTTCTATATGATGATTTTATTTATCTATATTCG 329
Db 273 AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTTTGA 332
QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTATGCGGATTCGAGATTTTGACGGTAAATTGAA 389
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTTAATGATGGGATTCAGATTTTAAATGTTCTGTACT 392
QY 390 AAATATATAGAGATTAATCTTTCTTATCTTTGGGGCTTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAACATATTTAGAGGCTCTCGGATAGCTGGAATAAGAAATCCTAATTTCTGCTC 452
QY 450 TCAAAAGACAATAATCTCTGATATCGGACAATTAGTTTATTTATTTAACTTTTCAGAAAG 509
Db 453 TGCTGAAGAACCTCGGTACTCGTTTTTAGAATCGCCGACTCAGAAATTTGTAGAAATTTAAC 512
QY 510 AGATTTCAATGAAATTTCTAGGAGGTCATTTGTCAAGAAACAATGCTCAAGTATTTCTTATT 569
Db 513 CGAGGGTCTTTAACGAATGGTGGCTCGTTAGTAGACAAAATGCCCAAAATATTTATTTATT 572
QY 570 ACCTACTTTTGCACAAGCTGCAAAATGTGCAGTTATTACTATTAAAGGGATGCAAGTTCAATA 629
Db 573 ACCTCTTTTTCGAGCGCTGTCATTTTCCATTTTATTACTACTAAGGGATGCTACTAGATA 632
QY 630 TAAAGACAATGGTTCCTCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCACTAAATTTGGGGGCTATACAAATGCTACACCTTTTATTAATTTATCAATCAAAACTAGT 692
QY 690 TAAAGAGTGTGTGATTTTACCGGTGATTACTATGAGCGATTTAAATATGCAAAACCGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
QY 750 GTATACCAATTAATGTTTATATTTGATTCAGGTAGGTTTAAATCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTATTGCGTACATTTGATAAATCGAGGTTTCAACGAACTTAAGACAACGAGG 767
QY 810 GACAGTCTGACACTTGGTGGAAATTTAAATAATTTGTTAGAGAAATGACGTTGGCGGT 869
Db 768 CACTAGTCTGACAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGAGATGACATGATGGT 827
QY 870 ATTGGATATTAATCGCTATATTTTCCAACTTATGATTTTCAGAAATATCCATTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTAACCAATAGAACAACA 887
QY 930 TGTAGAGTTGACTAGGGAAATTTATACAGATGCGAGTGGGATTTATCATCGGGAACTTATAG 989
Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATTTGTTTGTACATCGTAGTAGTCT 947
QY 990 TTGGTTACGGAATTTGGCCTTAATCTTTTAAATCG 1022
Db 948 TAGGGGAGAAAGTTGGTTTAGCTTTTGTAAATAG 980
```

RESULT 8

US-10-428-961-29

; Sequence 29, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MCO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-29

Query Match 7.7%; Score 160.6; DB 6; Length 2407;
Best Local Similarity 51.9%; Pred. No. 5.7e-26;
Matches 453; Conservative 0; Mismatches 369; Indels 51; Gaps 2;

QY 156 AATTGGGAATCAGTCGAAACGATAACAGATATGGGATAAAATCTTATAGAGTTTGTGAT 215
DB |||||
QY 153 AATAGGCGATGCAGCAAAAGACGATATCTATGGGCAACCATAGTCTCTCTATCAC 212
DB |||||
QY 216 AGAAGCTAGTTGGGTGGATTAATACACTATTAT-----CAATAATAGGAACCTAAT 269
DB |||||
QY 213 AGCACTTCTCTACTGGATTAATTAATAGTATATAGCTTTATAGGTAAAGTACTAGG 272
DB |||||
QY 270 TCCGACTAATCGTCGAACTGTCAGCACTTCTATATGTGATTTATATCTATAATTCG 329
DB |||||
QY 273 AGGTAGTAGGACATCCATATCAGATTTGCTATATGTGACTTATATCTATTTATGA 332
DB |||||
QY 330 TAAAGAGTAGCCGATAGTGTGTTTAAAGTAGCGATGCGATGCGATTTTGAACGGTAAATGAA 389
DB |||||
QY 333 TTTACGGGTAAAGTCAGAGTGTGTTTAAATGATGGATGCGATTTTAAATGTTCTGTACT 392
DB |||||
QY 390 AATATTAGAGATATATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 449
DB |||||
QY 393 CTTATACAGGAATATTTAGAGGCTCTGGATAGCTGGAATPAAGAACTCTAATTTCTGCTTC 452
DB |||||
QY 450 TCAAAAGACAAATAATCTGATATCGACAATAGTTTATTTTAAACTTTTCAGAAAG 509
DB |||||
QY 453 TGTGAAGAACTCGGTACTCGTTTAAAGTACGCGACTCGAATTTGTAGAAATTTTAAAC 512
DB |||||
QY 510 AGATTTCAATGAAATCTTAGGAGGGTCATTTGCAAGAAACAATGCTCAAGTATTTGTTAT 569
DB |||||
QY 513 CCGAGGTCCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCAAATATTTATTT 572
DB |||||
QY 570 ACCTACTTTTGCACAGCTGCAATGTCAGTTTATTTACTATTAAGGGATGCGAGTTCAATA 629
DB |||||
QY 573 ACCTCTTTTGGAGCGCTGCATTTTTCATTTTACTACTAAGGGATGCTACTAGATA 632
DB |||||
QY 630 TAAAGCACAAATGTTCCCATTTTGTAGTGCAGAGAATGTAAGATCGAAATTAATATCAC 689
DB |||||
QY 633 TGCACATTAATTTGGGGCTATACAACTGCTACACCTTTTAAATTTATCAATCAAACTAGT 692
DB |||||
QY 690 TAACAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTAATAATGCAAAACGGCAGA 749
DB |||||
QY 693 AGAGCTTATTT-----GAACT 707
DB |||||
QY 750 GTATACCAATTAATTTTATTTATTTGTTATCAGGTAGGTTTAAATCAGATAAACAGGGGG 809
DB |||||
QY 708 ATATACTGATTAATTTGGGTACATTTGGGATTAATCGAGGTTCACACCGAACTAAGCAACGAG 767
DB |||||

QY 810 GACAGGTGCTGACACACTTGGTCGAAATTTAATAAATTTCTGTAGAGAAATGACGTTGGCGGT 869
DB |||||
QY 768 GCCTAGTGTCTACAGCTTGGTTAGAAATTTCTAGATATCGAGAGAGATGACATTTGATGGG 827
DB |||||
QY 870 ATTGGATATTTATCGCTATATTTTCCAACTTATGATTTTGGAGAAATATCCATTTGCCAACACA 929
DB |||||
QY 828 ATTAGAAATAGTAGCATCATCTTTTCAAGTCTTGATATTAATCTAAATTTACCAATAGAAACAGA 887
DB |||||
QY 930 TGTAGAGTTCACCTAGGGAATTTATACAGATGAGTGGGATATTCATCGGGAACCTTATAG 989
DB |||||
QY 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCAATTTGGTTTGTATCATCGTAGTAGTCT 947
DB |||||
QY 990 TTGGTTACGGAATTTGGCCTAATAACTTTTAAATGG 1022
DB |||||
QY 948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAAATAG 980
DB |||||

RESULT 9

US-10-120-544A-19
; Sequence 19, Application US/10120544A
; Publication No. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/10/120,544A
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-10-120-544A-19

Query Match 4.9%; Score 102.4; DB 5; Length 4366;
Best Local Similarity 58.0%; Pred. No. 1.5e-12;
Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

QY 716 ATTACTATCAGCGATTTAAATGCAAAACGCGAGAGTATACCAATTTATTTTATATTGGT 775
DB |||||
QY 921 ATATTTACATCGCCNACAAAGAACTCCGCAACGTATGCAATCATTTGTACACTTGGT 980
DB |||||
QY 776 ATCAGGTAGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCCGAAT 835
DB |||||
QY 981 ATCAGACGGGTTTACA-----AAGATTCAAGGCGAGCGATGCTAGCAGTTGGGTCAA 1034
DB |||||
QY 836 TTAATAAATTTCTGTAGAGAAATGACGTTGGCGGTATTTGATATTTATTCCTATATTTCCAA 895
DB |||||
QY 1035 ATAAATCGATTTAGAGAGAAATAACGTTAAATAGTATTTGATATTTGTGCAATTTGTTTCAA 1094
DB |||||
QY 896 CTTATGATTTTTCAGAGAAATCCATTTGCCAACACATGTAGAGTTGACTAGCGAAATTTATA 955
DB |||||
QY 1095 ATATATGATGTTTGTAGTTATCAATACAGTTACGGGGAGAGCTTACGAGAGGAATTTATA 1154
DB |||||
QY 956 CAGATGCGAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAATTTGGCCTTAATCTT 1015
DB |||||
QY 1155 CGGATCCAGCAGTATATACGGGTACAGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1214
DB |||||


```
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-428-961-37

Query Match      4.6%; Score 95.6; DB 6; Length 4173;
Best Local Similarity 62.7%; Pred. No. 5.3e-11;
Matches 168; Conservative 0; Mismatches 94; Indels 6; Gaps 1;

QY 717 TTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATATTGTTTATTGTTA 776
Db 645 TTATTATGAGCGCAAGTGGAAACAACGAGAGATTATTCGCAATTATTCGTCAGATGGTA 704
QY 777 TCAGGTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTCGACACTTGGTCGAAATT 836
Db 705 TAATACAGGTCTAAATAGCTTGAGA-----GGGACAAATGCCGCAAGTTGGGTGCGTTA 758
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGGGTATTGGATATTATCGCTATATTTCCAAAC 896
Db 759 TAATCAATTCGTAGAGATCTACGTTAGGGGTATTAGATCTAGTGCACATATTCGCAAG 818
QY 897 TTATGATTTTGAGAAATATCCATGCGCAACATGATAGAGTTGCACTAGGGAAATTTATAC 956
Db 819 CTATGACACTCGCACTTATCCAAATAATACGAGTGCTCAGTTAAACAAGGGAAGTTTATAC 878
QY 957 AGATGAGTGGGATATTCATCGGGAAT 984
Db 879 AGACGCAATTTGGAGCAACAGGGGTAAAT 906

RESULT 13
US-10-120-544A-3
; Sequence 3, Application US/10120544A
; Publication No. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/10/120,544A
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-10-120-544A-3

Query Match      4.6%; Score 95.2; DB 5; Length 4359;
Best Local Similarity 62.0%; Pred. No. 6.7e-11;
Matches 170; Conservative 0; Mismatches 98; Indels 6; Gaps 1;

QY 696 TGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATAC 755
Db 1025 TGCTCAAGCTACTATTGACAATAATTAACAATGCCAAATAAGGAAACCGCAGAGTATGC 1084
QY 756 CAATTATTGTTTATATTGGTATCAGTAGGTTTAAATCAGATAAACAAGGGGGGACAGG 815
Db 1085 AAATCATTTGTACCACTTGGTATCAGCGGTTTTACA-----AAGATTGCAAGGCACTAC 1138
QY 816 TGCTGACACTTGGTCGAAATTTAAATAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGA 875
Db 1139 TGCTAGCAGTTGGCTCTCTTATCATAGATTTAGAACAGAGAAATGACACTAACAGTATTGGA 1198
QY 876 TATTATCGCTATATTTCACACTTATGATTTTGGAGAAATATCCATTGCCAACACATGTAGA 935
Db 1199 TATTTCGCGATTTATTTTCAAAATTTATGATGCCCGTAGTTACCCACTGGAGGTAAAGGGGAGA 1258
QY 936 GTTGACTAGGGAAATTTATACAGATGCAGTGGGA 969
Db 1259 GCTTACGAGAGAAATTTTATACGATCCAGTAGCA 1292

RESULT 14
US-11-091-654-3
; Sequence 3, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,654
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-654-3

Query Match      4.6%; Score 95.2; DB 10; Length 4359;
Best Local Similarity 62.0%; Pred. No. 6.7e-11;
Matches 170; Conservative 0; Mismatches 98; Indels 6; Gaps 1;

QY 696 TGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATAC 755
Db 1025 TGCTCAAGCTACTATTGACAATAATTAACAATGCCAAATAAGGAAACCGCAGAGTATGC 1084
QY 756 CAATTATTGTTTATATTGGTATCAGTAGGTTTAAATCAGATAAACAAGGGGGGACAGG 815
Db 1085 AAATCATTTGTACCACTTGGTATCAGCGGTTTTACA-----AAGATTGCAAGGCACTAC 1138
QY 816 TGCTGACACTTGGTCGAAATTTAAATAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGA 875
Db 1139 TGCTAGCAGTTGGCTCTCTTATCATAGATTTAGAACAGAGAAATGACACTAACAGTATTGGA 1198
QY 876 TATTATCGCTATATTTCACACTTATGATTTTGGAGAAATATCCATTGCCAACACATGTAGA 935
Db 1199 TATTTCGCGATTTATTTTCAAAATTTATGATGCCCGTAGTTACCCACTGGAGGTAAAGGGGAGA 1258
QY 936 GTTGACTAGGGAAATTTATACAGATGCAGTGGGA 969
Db 1259 GCTTACGAGAGAAATTTTATACGATCCAGTAGCA 1292
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RESULT 15
US-10-428-961-5
; Sequence 5, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201-1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-5

Query Match          4.5%; Score 94.4; DB 6; Length 1959;
Best Local Similarity 62.2%; Pred. No. 7.le-11;
Matches 168; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 716 ATTACTATGAGCGATTAAATGCAAAACGCGAGAGTATACCAATTATTGTTTATTGGT 775
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 AATATTACCGAGNACAAATCAGATATACAGAGGATATTCTAACCATTCGGTACATGGT 688

QY 776 ATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGGTGCTGACACTTGGTCGAAAT 835
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 689 ATAATACAGGGCTAAATAACTTAA-----GAGGGACAATGCTGAAAGTTGGTTGCGGT 742

QY 836 TTAATAAATTCGTAGAGAAATGACGTTGCGCGTATTGGATATTATCGCTATATTCCAA 895
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 743 ATAATCAATTCGCTAGAGACCTTAACGTTAGGGGTATTAGATTTAGTGGCCCTATTCCCAA 802

QY 896 CTTATGATTTTGAGAAATATCCATTGCCAACACATGATAGATTGACTAGGGAAATTTATA 955
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 803 GCTATGATACTCGCACTTATCCAATCAATACGAGTGCTCAGTTAACAGAGAAATTTATA 862

QY 956 CAGATCAGTGGGATATTTCATCGGGAAC TT 985
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Db 863 CAGATCCAATTGGGAGAACAAATGCACCTT 892
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Search completed: December 20, 2005, 04:49:20
Job time : 1035.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 14:38:00 ; Search time 135.839 Seconds
(without alignments)
7512.972 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaaagatgatgcata.....acgatctgttaccataa 2082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA New:*
- 1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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 - 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
 - 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
 - 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.4	4.9	4366	9	US-11-091-643-19
2	99.2	4.8	4119	7	US-11-070-575-4
3	95.2	4.6	4359	9	US-11-091-643-3
4	91.4	4.4	4188	9	US-11-091-643-5
5	87.8	4.2	1860	7	US-11-058-727-15
6	87.8	4.2	1860	7	US-11-108-389-15
7	87.8	4.2	1863	7	US-11-058-727-19
8	87.8	4.2	1863	7	US-11-108-389-19
9	87.8	4.2	2010	7	US-11-058-727-11
10	87.8	4.2	2010	7	US-11-108-389-11
11	87.8	4.2	2019	7	US-11-058-727-57
12	87.8	4.2	2019	7	US-11-058-727-59
13	87.8	4.2	2019	7	US-11-058-727-89
14	87.8	4.2	2019	7	US-11-058-727-91
15	87.8	4.2	2019	7	US-11-108-389-57
16	87.8	4.2	2019	7	US-11-108-389-59
17	87.8	4.2	2019	7	US-11-108-389-89
18	87.8	4.2	2019	7	US-11-108-389-91
19	87.8	4.2	2022	7	US-11-058-727-7
20	87.8	4.2	2022	7	US-11-058-727-21
21	87.8	4.2	2022	7	US-11-058-727-25
22	87.8	4.2	2022	7	US-11-058-727-29
23	87.8	4.2	2022	7	US-11-058-727-33

ALIGNMENTS

RESULT 1

US-11-091-643-19
; Sequence 19, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; FILE REFERENCE: poyucleotide encoding the same
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-643-19

Query Match 4.9%; Score 102.4; DB 9; Length 4366;

Best Local Similarity 58.0%; Pred. No. 2.6e+14;

Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

QY	716	ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTACCAATTTATTTTATTTGGT	775
DB	921	ATAATTACAATCGCAACAAAGAACTCGCAACGTCGCAATCATTTGTACAACTTGT	980
QY	776	ATCAGTAGGTTTAATTCAGATAAAACAGGGGGGACAGGTCTGACACTTGGTGAAT	835
DB	981	ATCAGCGGGTTTAC-----AAGATTGCAAGGCGAGTGTAGCAGTTGGTCAAAT	1034
QY	836	TTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATTTC	895


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; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4188
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4158)
US-11-091-643-5

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Query Match 4.4%; Score 91.4; DB 9; Length 4188;

Qy	715	GATTACTATGAGCGGATTAAATGCACAAACGCGCAGAGTATACCAATATTGTTTATTATGG	774
Db	766	GATAAATTATTAATCTCCAATTAAGCGCTCTGCAGATTATGCAAAATCATTTGTACAACTTGG	825
Qy	775	TATCAGGTAGCTTTAAATCAGATAAAACAGGGGGGACAGTGCTGCACATTTGGTCGAAA	834
Db	826	TATCGNCGGTTTACA-----AAGATTGCAAGGCCCAATGCTAGCAHTTGGGTCAAT	879
Qy	835	TTTAAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTTCCA	894
Db	880	TATAATTCGATTATAGAGAGAAATGACACTAACTGATTATAGATGTTTGTGCACTATTATTTCA	939
Qy	895	ACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTTGACTAGGGGAATTTAT	954
Db	940	AGTTATGATTATCGTAGTTACCCNATGGAGCTAAGGGGAGAGCTTACGAGAGAAATTTAT	999
Qy	955	ACAGATGCACTGGGATATTCATCGGGAACTTTATAG	989
Db	1000	ACGGATCCAGTAGAGGCTCTTTTGTGGTGAATAG	1034

RESULT 5

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US-11-058-727-15
/ Sequence 15, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnail
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
/ TITLE OF INVENTION: Activity
/ FILE REFERENCE: 357118/287809
/ CURRENT APPLICATION NUMBER: US/11/058,727
/ CURRENT FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15
/ LENGTH: 1860
/ TYPE: DNA
/ ORGANISM: Bacillus thuringiensis (truncated)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (10)...(1860)
/ FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-058-727-15

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Query Match 4.2%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6

Qy	714	TGATTACTATGAGCGATTAAATATGCAAAACGGCAGAGATATACCAATTATTTGTTATATTG	773
Db	555	TAACTATTATGATCGTCAAAATGAAACCTTACTGCAAGATATTCTGATCACTGCTGTAAGTG	614
Qy	774	GTATCAGGTAGGTTTAAATCAGATATAAACAAGGGGGGACAGTGCTGCACACTTGGTCGAA	833
Db	615	GTATGAACTGGTTTATGCAAAATTAANA-----GGCACGAGCGCTAAACAATGGTTCG	668
Qy	834	ATTTAATAAATTCGTTAGAGAAATGACGTTGCGCGGTATTGATATATTATCGCTATATTTCC	893
Db	669	CTATAACCAATTCGTTAGAGAAATGACACTGCGCGTTTTAGATGTTGTTGCAATTATTTCC	728
Qy	894	AACTTATGATTTTGAGAGAAATATCCATTGCCAACACATCTAGAGTTTGACTAGGGAATTTA	953
Db	729	AAATTATGACACACGACGTTACCCATTGAAACGAAGCACTAACACAGGGAAGTATA	788
Qy	954	TACAGATGCAGTGGGATATTATCATCGGAACTTATAGTTGGTTACGGAAT	1002
Db	789	TACAGATCCACTGGCGCGGTAAACAGTGCTCTTCAATTGGTTCCCTGGTAT	837

RESULT 6

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US-11-108-389-15
; Sequence 15, Application US/11108389
; Publication NO. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)....(1860)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15

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Query Match 4.2%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6

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; NAME/KEY: CDS
; LOCATION: (10)...(1860)
; FEATURE:

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QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773
Db 555 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATTCTGATCACTGTGTAAGTG 614
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGCTGACACTTGGTCGAA 833
Db 615 GTATGAAACTGGTTTATAGCAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 668
QY 834 ATTTTAATAATTTCTGATGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC 893
Db 669 CTATTAACCAATTCGCTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTATCCC 728
QY 894 AACTTATGATTTTGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 729 AAATTATGACACAGCGACGTACCCATGGAACGAAAGCACAACTAAACAAGGGAAGTATA 788
QY 954 TACAGATGACGTGGGATATTTCATCGGGAACCTTATAGTTGGTTACGGAAT 1002
Db 789 TACAGATCCACTGGGCGGTAAACGCTGTCTTCAATTGGTTCTCTGGTAT 837

RESULT 7

US-11-058-727-19
; Sequence 19, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1863)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: NGSr.N49PVD
US-11-058-727-19

Query Match 4.2%; Score 87.8; DB 7; Length 1863;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;
QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773
Db 558 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATTCTGATCACTGTGTAAGTG 617
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGCTGACACTTGGTCGAA 833
Db 618 GTATGAACTGGTTTATAGCAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 671

QY 834 ATTTTAATAATTTCTGATGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC 893
Db 672 CTATAACCAATTTCCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTATCCC 731
QY 894 AACTTATGATTTTGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 732 AAATTATGACACAGCGACGTACCCAAATGGAACGAAAGCACAACTTAAACAAGGGAAGTATA 791
QY 954 TACAGATGACGTGGGATATTTCATCGGGAACCTTATAGTTGGTTACGGAAT 1002
Db 792 TACAGATCCACTGGGCGGTAAACGCTGTCTTCAATTGGTTCTCTGGTAT 840

RESULT 8

US-11-108-389-19
; Sequence 19, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1863)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: NGSr.N49PVD
US-11-108-389-19

Query Match 4.2%; Score 87.8; DB 7; Length 1863;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;
QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773
Db 558 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATTCTGATCACTGTGTAAGTG 617
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGCTGACACTTGGTCGAA 833
Db 618 GTATGAACTGGTTTATAGCAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 671
QY 834 ATTTTAATAATTTCTGATGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC 893
Db 672 CTATAACCAATTTCCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTATCCC 731
QY 894 AACTTATGATTTTGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 732 AAATTATGACACAGCGACGTACCCAAATGGAACGAAAGCACAACTTAAACAAGGGAAGTATA 791

Qy 954 TACAGATGCAGTGGGATATTTCATCGGAACTTATAGTTGTTACCGAAT 1002
 Db 792 TACAGATCCACTGGGGCGGTAACGTCGTCTTCAATGGTTCTCTGGTAT 840

RESULT 9
US-11-058-727-11

Publication No. US20050261483A1

APPLICANT: Rafael Herrmann
APPLICANT: Theodore W Zahn

; APPLICANT: Billy Fred McCutchen
 ; APPLICANT: James K. Presnail

	TITLE OF INVENTION:	GENES ENCODING PROTEINS WITH PESTICIDAL ACTIVITY
1.	TITLE OF INVENTION:	ACTIVITY

;; CURRENT APPLICATION NUMBER: US/11/058,727
;; CURRENT FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/460,787

; PRIOR FILING DATE: 2003-06-25
 ;
 ; NUMBER OF SEQ ID NOS: 134
 ;

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; CRY IS NO 11
; LENGTH: 2010
TYPE: DNA

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;
; FEATURE:
; NAME/KEY: CDS

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0) - (0)

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US-11-058-727-11

Best local similarity 39.2%; Fied. NO. 4.3E-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1

687 TAACCTATTATGATCGTCAAATGAACTTACTGCAGAATATTCTGATCAGTGTGTAAGTG 746

[illegible]

Qy 834 ATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGCGTATTTATCGCTATATTTCC 893

Qy 894 AACTTATGATTTTGTGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAA

QY 954 TACAGATGCAGTGGGATATTTCATCGGGAACTTATAGTTGGTTACCGGAAT 1002

```
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-57

Query Match      4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTTG 773
Db 699 TAACTATTATGATCGTCAAACTTTACTGCAGATATTCTGATCACTGTGTAAGTG 758
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGTGTGACACTTTGGTCGAA 833
Db 759 GTATGAACTGTTTAGCAAAATTAATA-----GGCAGAGCGCTAAACAATGGTTGA 812
QY 834 ATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC 893
Db 813 CTATAACCAATTCGCTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTATTCCC 872
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 873 AAATTATGACACACGTACGTACCCAAATGGAACGAAACGACACAACTAACAGGGAAGTATA 932
QY 954 TACAGATGCGTGGGATATTTCATCGGGAACTTATAGTTGGTTTACGGAAT 1002
Db 933 TACAGATCCACTGGCGCGGTAAACGTGCTTCAATTGGTTCTCTGGTAT 981

RESULT 12
US-11-058-727-59
; Sequence 59, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)

US-11-058-727-89
; Sequence 89, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
```


US-11-058-727-89

Query Match 4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTG 773
DB 699 TAACTATTATGATCGTCAATGAACTTACTGCGAGAATATCTGATCACTGTGTAAAGTG 758

QY 774 GTATCAGGTAGTTTAAATCAGATAAAACAGGGGGGACAGTGCTGACACTTGGTGCAG 833
DB 759 GTATGAACACTGTTTAGCAAAATTAATA-----GGCACGAGCGCTAAACAATGGGTGA 812

QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGATATTATCGTATATTTC 893
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTAATTTCC 872

QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953
DB 873 AAATTATGACACATTAACGTAACCAATGGAACGAAAGCAACAACAAAGGGAAGTATA 932

QY 954 TACAGATGCGAGTGGGATATTATCGGGAACCTTATAGTTGGTTACGGAAT 1002
DB 933 TACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTGGTTCTCTGGGTAT 981

RESULT 14

US-11-058-727-91
; Sequence 91, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (2019)
US-11-058-727-91

Query Match 4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTG 773
DB 699 TAACTATTATGATCGTCAATGAACTTACTGCGAGAATATCTGATCACTGTGTAAAGTG 758

QY 774 GTATCAGGTAGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTGCAG 833

DB 759 GTATGAACACTGTTTAGCAAAATTAATA-----GGCACGAGCGCTAAACAATGGGTGA 812
QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGATATTATTCCTATATTTC 893
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTAATTTCC 872

QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953
DB 873 AAATTATGACACATTAACGTAACCAATGGAACGAAAGCAACAACAAAGGGAAGTATA 932

QY 954 TACAGATGCGAGTGGGATATTATCGGGAACCTTATAGTTGGTTACGGAAT 1002
DB 933 TACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTGGTTCTCTGGGTAT 981

RESULT 15

US-11-108-389-57
; Sequence 57, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (2019)
US-11-108-389-57

Query Match 4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTG 773
DB 699 TAACTATTATGATCGTCAATGAACTTACTGCGAGAATATCTGATCACTGTGTAAAGTG 758

QY 774 GTATCAGGTAGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTGCAG 833
DB 759 GTATGAACACTGTTTAGCAAAATTAATA-----GGCACGAGCGCTAAACAATGGGTGA 812

QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGATATTATTCCTATATTTC 893
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTAATTTCC 872

QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953
DB 873 AAATTATGACACATTAACGTAACCAATGGAACGAAAGCAACAACAAAGGGAAGTATA 932

QY 954 TACAGATGCGAGTGGGATATTATCGGGAACCTTATAGTTGGTTACGGAAT 1002

Db 933 TACAGATCCACTGGCGCGTAAACGTGTCTTCAATTGGTTCTCTGGTAT 981

Search completed: December 20, 2005, 04:58:17
Job time : 137.839 secs

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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:41:30 ; Search time 237.847 Seconds
(without alignments)
15559.937 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaagatgagtcacata.....acgatctgttaccacataa 2082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	168.6	8.1	3468	3	US-09-001-982-9
2	168.6	8.1	3468	3	US-09-668-650-9
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5	168.6	8.1	3471	3	US-10-099-285A-71
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7	168.6	8.1	3726	3	US-09-668-650-11
8	160.6	7.7	2407	3	US-09-661-322A-29
9	95.6	4.6	4173	3	US-09-661-322A-37
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12	93.4	4.5	3684	3	US-08-961-803-5
13	93.4	4.5	3684	3	US-09-661-322A-62
14	93	4.5	1561	2	US-08-532-547-2
15	93	4.5	1561	2	US-08-379-658B-2
16	93	4.5	1561	3	US-08-455-838-2
17	93	4.5	1561	3	US-09-019-809-2
18	93	4.5	1561	3	US-09-471-177-2
19	93	4.5	1561	3	US-09-220-806-2
20	93	4.5	1897	3	US-09-363-970-5
21	93	4.5	3471	3	US-09-002-285-73
22	93	4.5	3471	3	US-09-589-477-73
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26	93	4.5	4344	2	US-08-379-658B-4	Sequence 4, Appli
27	93	4.5	4344	3	US-08-455-838-4	Sequence 4, Appli
28	93	4.5	4344	3	US-09-019-809-4	Sequence 4, Appli
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31	92.8	4.5	3934	2	US-08-100-709-3	Sequence 3, Appli
32	92.8	4.5	3934	2	US-08-176-865-3	Sequence 3, Appli
33	92.8	4.5	3934	2	US-08-474-038-3	Sequence 3, Appli
34	92.8	4.5	3934	2	US-08-779-046-3	Sequence 3, Appli
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39	88.2	4.2	4074	2	US-08-377-690-1	Sequence 1, Appli
40	86.2	4.1	3507	2	US-08-315-468-3	Sequence 3, Appli
41	81.8	3.9	3504	3	US-10-089-678-2	Sequence 2, Appli
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43	79.6	3.8	1607	3	US-08-286-870A-5	Sequence 5, Appli
44	79.6	3.8	1946	3	US-08-286-870A-3	Sequence 3, Appli
45	79.6	3.8	2965	2	US-08-460-570-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-001-982-9
; Sequence 9, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3468

US-09-001-982-9

Query Match 8.1%; Score 168.6; DB 3; Length 3468;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
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DB 153 AATAGGCGATGCGAGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTCTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
DB 213 AGCACCTTCTTACTTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGTGATTTTATTTATCTATATTCG 329
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QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAGTGAATGCGATTCGAGATTTGACGGTAATAATTGAA 389
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QY 390 AAATATATAGAGTAGTATTAATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAAACCACT 449
DB 393 CTTATACAGAACTATTTAGAGGCTCTGGATAGCTGGAATAGAAATCCTAATCTGCTTC 452
QY 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATTTAGTTTATTTTAACTTTTCAGAAAG 509
DB 453 TCGTGAAGAACTCCGTACTCGTTTAAAGATCGCGACTCAGAAATTTGATAGAATTTTAAC 512
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DB 513 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCCAAATTTATTT 572
QY 570 ACTTCTTTTGACAGCTGCAAACTGTCAGTTTATTACTTAAAGGATGCGATTTCAATA 629
DB 573 ACTTCTTTTGAGCGCTGCAATTTTCCATTTATTACTTAAGGATGCTACTAGATA 632
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QY 870 ATTGATATATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTCGCAACACA 929
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QY 930 TGTAGAGTTGACTAGGGAATTTATACAGATGCGAGTGGGATTTTCAATCGGAACTTTATAG 989
DB 888 TTTTCAGTTGAGTAGGCTCATTTATACAGATCCAAATGGTTTGTGATCATCGTAGTGT 947
QY 990 TTTGGTTACGGAATTTGGCCTTAATCTTTTAAATGG 1022
DB 948 TAGGGGAGAAAGTTGGTTAGCTTTTGTAAATAG 980

RESULT 2
US-09-668-650-9
; Sequence 9, Application US/09668650
; Patent No. 6780408
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.

Stiekema, Willem J.
TITLE OF INVENTION: Hybrid Toxin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6780408artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/668,650
FILING DATE: 22-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/001,982
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/602,737
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3468
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-668-650-9

Query Match 8.1%; Score 168.6; DB 3; Length 3468;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTTGGGAATCAGTGCAGAACGATAACAAGTAGTTGGGATAAATCTTATAGAGTTTGTGAT 215
DB 153 AATAGGCGATGCGAGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
DB 213 AGCACCTTCTTACTTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGTGATTTTATTTATCTATATTCG 329
DB 273 AGGTAGTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATTTATCTATTATGA 332
QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTGAATGCGATTCGAGATTTGACGGTAATAATTGAA 389
DB 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGGATTCAGATTTTAAATGGTTCTGTACT 392
QY 390 AAATATATAGAGTAGTATTAATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAAACCACT 449
DB 393 CTTATACAGGAACTATTTAGAGGCTCTGGATAGCTGGAATAGAAATCCTAATTTCTGCTTC 452
QY 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATTTAGTTTATTTTAACTTTTCAGAAAG 509
DB 453 TCGTGAAGAACTCCCGTACTCGTTTAAAGATCGCGCACTCAGAAATTTGATAGAATTTTAAC 512

QY 510 AGATTTCATGAAATCTAGGAGGGTCATTGTCAAGAAACAAATGCTCAAGTATTGTTATT 569
Db 513 CCGAGGGCTTTAAACAAATGGTGGCTCGTTAGCTAGACAAATGCCAAATATTATTATT 572
QY 570 ACTTACTTTTGCACAAAGCTGCAAAATGTCAGTATTACTATTAAAGGATGCGAGTTCAAATA 629
Db 573 ACCTTCTTTTGGAGCGCTGCATTTTTCATTTTCCATTTTACTACTAAAGGATGCTACTAGATA 632
QY 630 TAAAGCACATGTTCCCATTTTGTAGTCAGAGATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCCTAAATGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
QY 750 GTATACCAATATTGTTTATATTGTTATCGAGTATGAGTAAATTCAGATAAAACAGGGGG 809
Db 708 ATATAGTATGATTTGGTACATTTGTTATGATGATGATGATGATGATGATGATGATGAT 767
QY 810 GACAGTGTGACACATGCTGCAAAATTTAAATTTTCGTAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTCATAGATATCGTAGAGATGACATTGATGTT 827
QY 870 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCTTCAAGTCTTGATATTACTAATACCAATAGAAACAGA 887
QY 930 TGTAGAGTGTAGGAAATTTATACAGATGAGTGGGATATTATCGGGAATTTATAG 989
Db 888 TTTTCAGTTGAGTAGGGTCAITTTATACAGATCCAATTTGGTTTGTACATCGTAGTCT 947
QY 990 TGTGTTACGGATTGCGCTAACTTTTAAATG 1022
Db 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAAATAG 980

RESULT 3

US-09-002-285-71
; Sequence 71, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/896,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-002-285-71

Query Match 8.1%; Score 168.6; DB 3; Length 3471;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTTGGGAATCAGTCGAAACGATACACAGTATTCGGATATAATCTTATAGAGTTTCTGAT 215
Db 153 AATAGCGGATGAGCAAAAGAGCAGTATCTATTGGGCAACACATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT 269
Db 213 AGCACTTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACTGTCAGCACTTTCTATATGTGATTTATTTATCTATAATTCG 329
Db 273 AGGTAGTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTATGA 332
QY 330 TAAAGAGGTAGCGGATGATGTTTAAAGTATCGGATTCGAGATTTTGACGGTAAATGAA 389
Db 333 TTTACGGGTAGTCAGAGTGTTTTAAATGATGGGATTCAGATTTTAAATGTTCTGTACT 392
QY 390 AAATATATAGAGATATTATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAATCTTTTAGAGCTCTGGATAGCTGGAATAAGATCCCTAATTTCTGCTTC 452
QY 450 TCAAAAGACAAATAATTCGTATATCGGACAATTAGTTTATTTATTTTAACTTTTCAGAAAG 509
Db 453 TGTGAAGAACTCCGTACTCGTTTGAATCGCGACTCAGAATTTGATAGAATTTTAAAC 512
QY 510 AGATTTCAATGAATTTCTAGGAGGCTCATTTGCAAGAAACAATGCTCAAGTATTGTTATT 569
Db 513 CCGAGGCTTTTAAACGAATGTTGGTGGCTGTAGCTAGACAAAATGCCAAATATTATTATT 572
QY 570 ACTTACTTTTGCACAAAGCTGCAAAATGTGCAGTATTACTATTAAAGGATGCGAGTTCATA 629
Db 573 ACCTTCTTTTGGAGGCTGCAATTTTCCATTTTATCTACTAGGATGCTACTAGATA 632
QY 630 TAAAGCAAAATGTTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCCTAAATGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTAAAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
QY 750 GTATACCAATATTGTTTATATTGTTATCGAGTATGAGTAAATTCAGATAAAACAGGGGG 809
Db 708 ATATAGTATGATTTGGTACATTTGTTATATCGAGGTTTCAACGAACTAAGACACAGG 767
QY 810 GACAGTGTGACACTTGGTCCAAATTTTAAATTTTTCGTAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTTTCAATAGATATCGTAGAGATGACATTGATGTT 827
QY 870 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCTTCAAGTCTTGATATTACTAATACCAATAGAAACAGA 887
QY 930 TGTAGAGTGTAGGAAATTTTATACAGATGAGTGGGATATTATCGGGAATTTATAG 989

Db 888 TTTTCAGTTGAGTAGGTCATTATATACAGATCCAAATGGTTTGTATACATCGTAGTCT 947
QY 990 TTGGTTACGGAATTGGCCCTAACTATTTTAATGG 1022
Db 948 TAGGGGAGAAAGTTGGTTAGCTTGTATATAG 980

RESULT 4

US-09-589-477-71
; Sequence 71, Application US/09589477
; Patent No. 6570005
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-589-477-71

Query Match 8.1%; Score 168.6; DB 3; Length 3471;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTGGGAATCAGTCGAACGATACAAAGTATGGGATAAATCTTATAGAGTTTGTGAT 215
Db 153 ATAGCGGATGAGCAAAAGAGCAGTATCTATTGGGACAAACCATAGTCTCTTATAC 212
QY 216 AGAACCTAGTTGGGTGGGAATTAATACATTTAT-----CAATAATAGGAAACTAAT 269
Db 213 AGCACCTTCTCTTACTGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACGTGTGCAGCACTTCTCTATATGTGATTATATCTATAATTCG 329

Db 273 AGGTAGTAGTGACAATCCATATCAGATTTGTCTATATGTGACTTATTTATCTATTATGA 332
QY 330 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTATGCGATTCAGATTTTGAAGGTAATTTGAA 389
Db 333 TTTACGGGTAGTCAGAGTGTGTTTAAATGATGGGATTCAGATTTTAAATGTTCTGTACT 392
QY 390 AAAATTATAGAGATTTATCTTTCTTATCTTTGGGCTTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAATCTTTAGAGGCTCTGGATAGCTGGAATAAGAAATCCTAAATCTGCTTC 452
QY 450 TCAAAAGACAAATAATCTCTGATATCGGACAATTAGTTTATTTATTTAAACTTTTCAGAAAG 509
Db 453 TGCTGAAGAATCTCGGTACTCGTTTGTAGAAATCGCGACTCAGAAATTTGTAGAAATTTAAAC 512
QY 510 AGATTTCAATGAAATCTTAGGAGGCTCATTTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569
Db 513 CCGAGGCTCTTTACGAATGGTGGCTCGTTAGCTAGACAAATGCGCAATATTTATTTATT 572
QY 570 ACCTACTTTTGCACAAAGCTGCAAAATGTCAGTTTATTTACTTATTAAGGGATGCAAGTTCAATA 629
Db 573 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTTACTTACTTAAAGGATGCTACTAGATA 632
QY 630 TAAAGCACAAATGGTTCCTCATTTTTCAGTGCAGAGATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCACTAATTTGGGGCTATACAATGCTACACCTTTTATTAATTTATCAATCAAACTAGT 692
QY 690 TAAAGTGTGTGATTTTACCGGTGATTTACTATGAGCGATTTAAAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
QY 750 GTATACCAATTTTGTATTTTATATTTGATATCAGTATAGTTTAAATCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTATTGCGTACATTTGATAAATCGAGGTTTCAACGAATTAAGACAACGAGG 767
QY 810 GACAGTCTGACACTTGGTGAATTTTAAATAATTTGCTAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTCTACAGCTTGGTTAGAAATTTCTAGATATCGTAGAGATGACATTTGATGGT 827
QY 870 ATTGATATTTATCGCTATATTTTCCAACTTTATGATTTTGAAGAAATATCCATTGCCCAACACA 929
Db 828 ATTAGATATAGTATCATCTTTTCAAGTCTTGATATTTACTAATTTACCAATAGAAACAGA 887
QY 930 TGTAGATGACTAGGAAATTTATACAGATGCAAGTGGGATATTCATCGGGAACCTTTATAG 989
Db 888 TTTTCAGTTGAGTAGGGTCAITTTATACAGATCCAAATGGTTTGTGTACATCGTAGTGTCT 947
QY 990 TTGGTTACGGAATTTGGCTTAATCTTTTAATGG 1022
Db 948 TAGGGGAGAAAGTTGGTTTAGCTTTGTTAATAG 980

RESULT 5

US-10-099-285A-71
; Sequence 71, Application US/10099285A
; Patent No. 6752992
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; Wicker, Carol
; Narva, Kenneth E.
; Walz, Michelle
; Stockhoff, Brian
; Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:


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Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTGGGAATCAGTCGAACGATAAAGATATGGGATAATCTTATAGATTTGTGAT 215
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Db 153 AATAGCGGATGACGACAAAGACAGTATCTATGGGACACCATAGTCTCTTTATCAC 212
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QY 216 AGAACCTAGCTTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
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Db 213 AGACCTTCTCTTACTGGGAATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
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QY 270 TCCGACTAATCGTCAAACTGTGTGACGACCTTTCTATATGTGATTTTATCTATATAATTCG 329
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Db 273 AGGTAGTAGTGGCAATCCATACAGATTTGCTATATGTGACTTATCTATTATTGA 332
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QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTATGCGATGCGAGATTTTGACGGTAAATGAA 389
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Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGATGCGAGATTTTAAATGGTCTGTACT 392
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QY 390 AAATTATAGAGATATTATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAACCACT 449
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Db 393 CTTATACAGGAATTTTAGAGCTCTGGATAGCTGGAATAAGAAATCCTAATTCGTCTTC 452
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QY 450 TCAAAAGACAAATAATTCGTATATCGGCAATTAGTTTATTTTAAACTTTTCAGAAAG 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 TGCTGAAGACTCCGCTACTCGTTTAGAATCGCGACTCAGAAATTTGATAGAAATTTAAAC 512
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QY 510 AGATTTCAATGAAATTTCTAGGAGGTCTATTGTCAAGAAACAATGCTCAAGTATTGTATT 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGCAAAATGCCAAATATTATTATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 570 ACTTACTTTTGCACAGCTGCAATGTGCGATTTACTATTAAAGGATGCGATTCAATA 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 ACCTTCTTTTGGAGCGCTGCATTTTTCATTTTACTTAAAGGGATGCTACTAGATA 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 630 TAAAGCACAAATGTTCCCAATTTTGGATGCGAGAAATGAAGATCGGAATTAATATCACC 689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 TGGCACTAATTTGGGGCTATACATGCTACACCTTTTATTAATTTATCAATCAAACTAGT 692
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QY 690 TAACAGTGTGTGATTTTACCAGGTGATTTACTATAGCGGATTAATAATGCAAAACGCGAGA 749
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Db 693 AGAGCTTAT-----GAACT 707
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QY 750 GTATACCAATATTGTTTATATTTGTTATCGATCAGGTAGGTTTAAATCAGATAAAACAGGGGG 809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 ATATACTGAATTTGCGTACATTTGTTAATATCGAGGTTTCAACGAACTAAGAACACGAGG 767
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 810 GACAGTGTGACACATTTGCTCGAAATTTAAATAAATTCGTAGAGAAATGACGTTGGCGGT 869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTCATAGATATCGTAGAGATGACATTTGATGT 827
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 870 ATTGGATATTATCGCTATATTTCCAACTATGATTTTGAAGAATATPCCATTCGCAACACA 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTTACCCAATAGAAACAGA 887
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QY 930 TGTAGATTGACTTAGGGAATTTATACAGATGCGATGGGATATTATCGGGAACTTATAG 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 888 TTTTCAGTTGAGTAGGGTCAITTTATACAGATCAATTTGGTTTGTGATCATCGTAGTGTCT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 990 TTGGTTTACGGAATTTGGCTTAATACTTTTAAATGG 1022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 948 TAGGGGGAAGATTGGTTTAGCTTTGTTAATAG 980
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RESULT 7
US-09-668-650-11
; Sequence 11, Application US/09668650
; Patent No. 6780408
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: No. 6780408artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/668,650  
; FILING DATE: 22-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,982  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/602,737  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3726 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..3726  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-668-650-11
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Query Match 8.1%; Score 168.6; DB 3; Length 3726;  
Best Local Similarity 52.5%; Pred. No. 1.9e-30;  
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;  
QY 156 AATTGGGAATCAGTCGAACGATAAAGATATGGGATAAATCTTATAGATTTGTGAT 215  
Db 153 AATAGCGGATGACGACAAAGACAGTATCTATGGGACACCATAGTCTCTTTATCAC 212  
QY 216 AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269  
Db 213 AGACCTTCTCTTACTGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272  
QY 270 TCCGACTAATCGTCAAACTGTGTGACGACCTTTCTATATGTGATTTTATCTATATAATTCG 329  
Db 273 AGGTAGTAGTGGCAATCCATACAGATTTGCTATATGTGACTTATCTATTATTGA 332  
QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTATGCGATGCGAGATTTTGACGGTAAATGAA 389  
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGGATGCGAGATTTTAAATGGTCTGTACT 392  
QY 390 AAATTATAGAGATATTATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAACCACT 449  
Db 393 CTTATACAGGAATTTTAGAGCTCTGGATAGCTGGAATAAGAAATCCTAATTCGTCTTC 452  
QY 450 TCAAAAGACAAATAATTCGTATATCGGCAATTAGTTTATTTTAAACTTTTCAGAAAG 509  
Db 453 TGCTGAAGACTCCGCTACTCGTTTAGAATCGCGACTCAGAAATTTGATAGAAATTTAAAC 512  
QY 510 AGATTTCAATGAAATTTCTAGGAGGTCTATTGTCAAGAAACAATGCTCAAGTATTGTATT 569  
Db 513 CCGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGCAAAATGCCAAATATTATTATT 572  
QY 570 ACTTACTTTTGCACAGCTGCAATGTGCGATTTACTATTAAAGGATGCGATTCAATA 629
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Db 573 ACCTCTCTTTGCGAGCGTGCATTTTCCATTTTATTTACTACTAAAGGATGCTACTAGATA 632
Qy 630 TAAAGCACATGTTCCCATTTTGGAGTCAGAGATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCATAATTTGGGGCTATACAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
Qy 690 TAAAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACCAATTAATTTTATTTATTTGGTATCAGGTAGTTTAAATTCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTAATTTGGTACATTTGTAATTCAGTCTTGATATTAATTAATTAATTAATTA 887
Qy 930 TGTAGAGTGTACAGGAAATTTATACAGATCGAGTGGGATATTCATCGGGAATTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAAATTTGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGGAATTTGCTTAATTTTAAATG 1022
Db 948 TAGGGAGAAAGTTGGTTTGGTTTAAATAG 980
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RESULT 8

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US-09-661-322A-29
; Sequence 29, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-29
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Query Match 7.7%; Score 160.6; DB 3; Length 2407;
Best Local Similarity 51.9%; Pred. No. 1.4e-28; Indels 51; Gaps 2;
Matches 453; Conservative 0; Mismatches 369;

Qy 156 AATTTGGGAATCAGTCGAAACGATAACAAGTATTTGGGATAAATCTTTATAGAGTTTGTGAT 215
Db 153 AATAGCGATGCGAGCAAAAGAGCAGTATCTATTGGGACACCATAGTCTCTTTATCAC 212
Qy 216 AGAACCTAGTTGGGTGGGAATTAATACACTATTAT-----CAATTAATAGGAAACTAAT 269
Db 213 AGCACCTCTCTTACTGGAATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272
Qy 270 TCCGACTAATCGTCAACATGTCGACACTTTCTATATGATTTATTTATTTATTTATTTATTCG 329
Db 273 AGGTAGTGTGGACAATCCATATCAGATTTGCTATATGACTTATATCTATTATTTATTA 332
Qy 330 TAAAGAGGTAGCGCATAGTGTGTTTAAAGTGTGCGATTGCGAGATTTTGGCGGTAATTTGAA 389
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Db 333 TTTACGGTAACTCAGAGTGTTTTAAATGATGGATTCAGAGATTTTAAATGTTCTGTA 392
Qy 390 AAATTTATAGAGATTAATATCTTTCTTATCTTCGGGGCTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAATCTATTTAGAGGCTCTGGATAGCTGGAATTAAGAAATCCCTAAATTCGCTTC 452
Qy 450 TCAAAAGACAAAATAATCTCTGATATCGGACAAATTAGTTTATTTATTTTAAACTTTTCAGAAAG 509
Db 453 TGCTGAGAACTCCGCTACTCGTTTGTAGATCCCGACTCAGAAATTTGATAGAAATTTTAAAC 512
Qy 510 AGATTTCAATGAATTTCTAGGAGGTCATTTGTCAAGAAAACAATGCTCAAGATATTTGTTAT 569
Db 513 CCGAGGCTCTTTAAACGAATGTTGGCTCGTTAGTAGACAAAATGCCCAAATATTTATTT 572
Qy 570 ACTACTTTTGCACAAGCTGCAAAATGTCAGTATTTACTATTTAAGGATGCAAGTTCAATA 629
Db 573 ACCTCTCTTTTGGAGCGCTGCATTTTCCATTTTATTTACTACTAAGGATGCTACTAGNTA 632
Qy 630 TAAAGCACAAATGTTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTTAATATCACC 689
Db 633 TGGCATAATTTGGGGCTATACAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692
Qy 690 TAAAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTAAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACCAATTAATTTTATTTATTTGGTATCAGGTAGTTTAAATTCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTAATTTGGTACATTTGGGATAATTCAGGTTTCAACCGAATTAAGACAACGAG 767
Qy 810 GACAGTGTCTGACACTTTGGTCGAAATTTAAATAAATTTTCGTAGAGAAATCAGCTTGGCGGT 869
Db 768 GCCTAGTGTACAGCTTTGGTTAGAAATTTCAATAGATTCGAGAGAGATGACATTTGATGG 827
Qy 870 ATTGATATTAATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCAATTTCAAGTCTTGATATTAATTAATTAATTAATTAATTAATTA 989
Qy 930 TGTAGAGTGTACAGGAAATTTATACAGATCGAGTGGGATATTCATCGGGAATTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAAATTTGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGGAATTTGCTTAATTTTAAATG 1022
Db 948 TAGGGAGAAAGTTGGTTTGGTTTAAATAG 980
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RESULT 9

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US-09-661-322A-37
; Sequence 37, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 4173
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-09-661-322A-37
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Query Match 4.6%; Score 95.6; DB 3; Length 4173;
Best Local Similarity 62.7%; Pred. No. 4.6e-13;
Matches 168; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
QY 717 TTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGTA 776
Db 645 TTATTATGAGCGCAAGTGGAAACAGAGATATTCCGACTATTGCGTAGAATGGTA 704
QY 777 TCAGGTAGGTTTAAATFCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 836
Db 705 TAATACAGGTCTAAATAGCTTGAGA-----GGGACAAATGCGCAAGTTGGTGGTTA 758
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTCCAAAC 896
Db 759 TAATCAATTTCCGTAGAGATCTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAG 818
QY 897 TTATGATTTTGAGAAATATCCATTGCGCAACACATGTPAGAGTTGACCTAGGGAATTTATAC 956
Db 819 CTATGACACTCGCACTTATCCAAATAAATAGAGTGTCTAGTTAAACAGGGAAGTTTATAC 878
QY 957 AGATCGAGTGGGATATTTCATCGGGAAT 984
Db 879 AGACGCAATTGGAGCAACAGGGTAAAT 906

RESULT 10
US-09-661-322A-5
; Sequence 5, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-5

Query Match 4.5%; Score 94.4; DB 3; Length 1959;
Best Local Similarity 62.2%; Pred. No. 7.5e-13;
Matches 168; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 716 ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGTT 775
Db 629 ATATTACAGGACAAATCAGATATACAGAGATATTCTAACCAATTCGTCACATGT 688
QY 776 ATCAGGTAGGTTTAAATFCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 835
Db 689 ATAATACAGGGCTAAATACTTAA-----GAGGGACAAATGCTGAAAGTTGGTTCGGT 742
QY 836 TTAATAAATTTCTAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCNA 895
Db 743 ATAATCAATTTCCGTAGAGACCTTAACGTTAGGGGTATTAGATTAGTAGCCCTATTCCCAA 802
QY 896 CTTATGATTTGAGAAATATCCATTGCGCAACACATGATAGTTGACTAGGGAATTTATA 955
Db 803 GCTATGATACTCGCACTTATCCAAATAACAGAGTGTCTAGTTAAACAGAGAAATTTATA 862
QY 956 CAGATCGAGTGGGATATTTCATCGGGAATTT 985
Db 863 CAGATCCAATTTGGGAAACAAATGCACCTT 892

RESULT 11
US-08-448-170-7
; Sequence 7, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-170-7

Query Match 4.5%; Score 93.4; DB 2; Length 3684;
Best Local Similarity 62.1%; Pred. No. 1.5e-12;
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 717 TTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGTA 776
Db 645 TTATTATGAGCGCAAGTGGAAACAGAGATATTCTGATTTATTCGCAAGATGGTA 704
QY 777 TCAGGTAGGTTTAAATFCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 836
Db 705 TAATACAGGGTTTAAATAATTTGAGA-----GGGACAAATGCTGAAAGTTGGTTCGGATA 758
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCCAAC 896
Db 759 TAATCAATTTCCGTAGAGACTTAAACGCTAGGAGTATTAGATCTAGTGGCACTATTTCCTCAAG 818
QY 897 TTATGATTTTGAGAAATATCCATTGCGCAACACATGATAGTTGACTAGGGAATTTATAC 956
Db 819 CTATGACAGCGGTGTTTATCCAAATGAATACAGTGTCTCAATTAAACAGAGAAATTTATAC 878

QY 957 AGATGCGTGGGATATTCATCGGGAACCTT 985
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Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907
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RESULT 12

US-08-961-803-5
; Sequence 5, Application US/089961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 615058961 Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: N/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-961-803-5

Query Match 4.5%; Score 93.4; DB 3; Length 3684;
Best Local Similarity 62.1%; Pred. No. 1.5e-12;
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 717 TTACTATGACGATTAAATGCAAAACGCGCAGAGTATACCAATATTGTTATTATGGTA 776
|||||
Db 645 TTATTATGAGCGCCAAAGTGGAAAAACGAGAGATATCTGATTATGCGCAAGATGGTA 704
|||||
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGCGACAGGTGCTGACACTTTGGTCGAAATT 836
|||||

Db 705 TAATACGGGTTTAAATAATTTGAGA-----GGACAAATGCTGAAAGTTGGTTGCGATA 758
|||||
QY 837 TAATAAATTTCTGTAGAGAAATGACGTTGGGGTATTGGATATATTCGCTATATTTTCCAAC 896
|||||
Db 759 TAATCAATTTCCGTAGAGACTTAAACGCTAGGAGTATTAGATCTAGTGGCACTATTTCCCAAG 818
|||||
QY 897 TTATGATTTTGGAGAAATATCCATTGCGCAACACATGTAGAGTTGACATAGGGAATTTTATAC 956
|||||
Db 819 CTATGACACGCGTGTATTCCAAATGAATCAAGTCTCAATTAAACAAGAAATTTTATAC 878
|||||
QY 957 AGATGCGTGGGATATTCATCGGGAACCTT 985
|||||
Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907
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RESULT 13

US-09-661-322A-62
; Sequence 62, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 62
; LENGTH: 3684
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-661-322A-62

Query Match 4.5%; Score 93.4; DB 3; Length 3684;
Best Local Similarity 62.1%; Pred. No. 1.5e-12;
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 717 TTACTATGACGATTAAATGCAAAACGCGCAGAGTATACCAATATTGTTATTATGGTA 776
|||||
Db 645 TTATTATGAGCGCCAAAGTGGAAAAACGAGAGATATCTGATTATGCGCAAGATGGTA 704
|||||
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGCGACAGGTGCTGACACTTTGGTCGAAATT 836
|||||
Db 705 TAATACGGGTTTAAATAATTTGAGA-----GGACAAATGCTGAAAGTTGGTTGCGATA 758
|||||
QY 837 TAATAAATTTCTGTAGAGAAATGACGTTGGGGTATTGGATATATTCGCTATATTTTCCAAC 896
|||||
Db 759 TAATCAATTTCCGTAGAGACTTAAACGCTAGGAGTATTAGATCTAGTGGCACTATTTCCCAAG 818
|||||
QY 897 TTATGATTTTGGAGAAATATCCATTGCGCAACACATGTAGAGTTGACATAGGGAATTTTATAC 956
|||||
Db 819 CTATGACACGCGTGTATTCCAAATGAATCAAGTCTCAATTAAACAAGAAATTTTATAC 878
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QY 957 AGATGCGTGGGATATTCATCGGGAACCTT 985
|||||
Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907
|||||

RESULT 14

US-08-532-547-2
; Sequence 2, Application US/08532547
; Patent No. 5861543
; GENERAL INFORMATION:
; APPLICANT: LAMBERT, BART
; APPLICANT: JANSSENS, STEFAN
; APPLICANT: VAN AUDENHOVE, KATRIEN
; APPLICANT: PEPEROEN, MARNIX

```

; APPLICANT: VAN RIE, JEROEN
; APPLICANT: VAN AARSEN, ROEL
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIR
; TITLE OF INVENTION: INSECTICIDAL PROTEINS.
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,547
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-109P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Bacillus thuringiensis
; STRAIN: BTS02618A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1561
; OTHER INFORMATION: /note= "contains the translation
; OTHER INFORMATION: initiation codon of the BTS02618A gene"
;
US-08-532-547-2

Query Match 4.5%; Score 93; DB 2; Length 1561;
Best Local Similarity 61.5%; Pred. No. 1.5e-12;
Matches 169; Conservative 0; Mismatches 100; Indels 6; Gaps 1;

QY 718 TACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTGGTAT 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
885 TATTATGACCGTCAATTGGAACCTAACCGCTAAGTACACTAATTACTGTGAAACTTGGTAT 944
QY 778 CAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTT 837
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
945 AATACAGGTTTAGATCGTTTAAAGA-----GGAACAAATACTGAAAGTTGGTTAAGATAT 998
QY 838 AATAAATTTTCGTAGAGAAATGAGTTGGCGGTATTGGATATTATCGCTATATTTCCAACT 897
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
999 CATCAATTCGTAGAGAAATGACTTTAGTGGTATTAGATGTTGTGGCGCTATTTCCATAT 1058
QY 898 TATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTTATACA 957
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1059 TATGATGTACGACTTTATCCACGGGATCAAAACCCACAGCTTACAGCTGAGGTATATACA 1118
QY 958 GATCGAGTGGATATTCATCGGGAACCTTATGTTG 992
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1119 GATCCGATTGTATTTAATCCACACGACTAATGTTGG 1153

RESULT 15
US-08-379-656B-2
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; Sequence 2, Application US/08379656B
; Patent No. 5885571
; GENERAL INFORMATION:
; APPLICANT: Lambert Bart
; APPLICANT: Jansens, Stefan
; APPLICANT: Van Audenhove, Katrien
; APPLICANT: Peferoen, Marnix
; TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
; TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,656B
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/01820
; FILING DATE: 12-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93400949.9
; FILING DATE: 09-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92402358.8
; FILING DATE: 27-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-104P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: BTS02618A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1561
; OTHER INFORMATION: /note= "contains the translation
; OTHER INFORMATION: initiation codon of the BTS02618A gene"
;
US-08-379-656B-2

Query Match 4.5%; Score 93; DB 2; Length 1561;
Best Local Similarity 61.5%; Pred. No. 1.5e-12;
Matches 169; Conservative 0; Mismatches 100; Indels 6; Gaps 1;

QY 718 TACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTGGTAT 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
885 TATTATGACCGTCAATTGGAACCTAACCGCTAAGTACACTAATTACTGTGAAACTTGGTAT 944
QY 778 CAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTT 837
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
945 AATACAGGTTTAGATCGTTTAAAGA-----GGAACAAATACTGAAAGTTGGTTAAGATAT 998

RESULT 15
US-08-379-656B-2
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